



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 96696**

**TO: Medina A Ibrahim  
Location: CM1/9E03/9E12  
Art Unit: 1638  
Monday, June 23, 2003**

**Case Serial Number: 010731**

**From: Edward Hart  
Location: Biotech-Chem Library  
CM1-6B02  
Phone: 305-9203**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Ibrahim,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 04:26:33 ; Search time 1133 Seconds

(without alignments)  
6421.625 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250

Sequence: 1 GGGGATCCCAATCTAATCA.....AAAAGATCTAAGATCCCC 250

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_da:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_ph:\*
- 7: gb\_pi:\*
- 8: gb\_pi:\*
- 9: gb\_pi:\*
- 10: gb\_pi:\*
- 11: gb\_pi:\*
- 12: gb\_pi:\*
- 13: gb\_pi:\*
- 14: gb\_pi:\*
- 15: gb\_pi:\*
- 16: gb\_pi:\*
- 17: gb\_pi:\*
- 18: gb\_pi:\*
- 19: gb\_pi:\*
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- 31: gb\_pi:\*
- 32: gb\_pi:\*
- 33: gb\_pi:\*
- 34: gb\_pi:\*
- 35: gb\_pi:\*
- 36: gb\_pi:\*
- 37: gb\_pi:\*
- 38: gb\_pi:\*
- 39: gb\_pi:\*
- 40: gb\_pi:\*
- 41: gb\_pi:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	234	93.6	406	8	AF319468	AF319468 Medicago
2	156.4	62.6	468	8	PEADRR230A	L01578 Pea (p1230)
3	156.4	62.6	468	8	PSPI230	X52225 P.sativum p
4	154.8	61.9	363	8	AF139018	AF139018 Pisum sat
5	119.4	47.8	494	6	AX252303	AX252303 Sequence
6	113	45.2	496	8	AB020613	AB020613 Vigna rad
7	109.8	43.9	459	8	VUSTORED	X16877 Vigna ungu
8	98	39.2	456	8	PEADRR230B	L01579 Pisum sativ
9	98	39.2	456	8	PSPI39	X52224 P.sativum p
10	49.2	19.7	380	8	AB049718	AB049718 Pisum sat
11	41.8	16.7	922	8	MTNIGENE	Y10456 Medicago tr
12	40	16.0	141	6	A27063	A27063 L.cicera AF
13	40	16.0	141	6	A39547	A39547 Sequence 35
14	40	16.0	141	6	AR050147	AR050147 Sequence
15	40	16.0	141	6	AR130266	AR130266 Sequence
16	40	16.0	141	6	I23722	I23722 Sequence 35
17	38.2	15.3	200218	2	AC123956	AC123956 Mus muscu
18	38.2	15.3	206082	2	AC126936	AC126936 Mus muscu
19	38	15.2	281	8	AF293407	AF293407 Phaseolus
20	37.8	15.1	170559	2	AC026989	AC026989 Homo sapi
21	37.8	15.1	182997	2	AL355332	AL355332 Human DNA
22	37.6	15.0	133418	9	AL353709	AL353709 Human DNA
23	37.6	15.0	157812	2	AC055805	AC055805 Homo sapi
24	37.4	15.0	68912	9	AC097490	AC097490 Homo sapi
25	37.4	15.0	138868	2	AC079302	AC079302 Homo sapi
26	37.2	14.9	134286	9	AC025771	AC025771 Homo sapi
27	37.2	14.9	170272	9	AC024589	AC024589 Homo sapi
28	36	14.4	170670	2	AC121758	AC121758 Homo sapi
29	36	14.4	171998	9	AC026120	AC026120 Homo sapi
30	36	14.4	198695	10	AC090648	AC090648 Genomic s
31	36	14.4	212722	2	AC087158	AC087158 Mus muscu
32	36	14.4	223412	2	AC124722	AC124722 Mus muscu
33	35.6	14.2	130754	2	AC093325	AC093325 Homo sapi
34	35.6	14.2	152779	2	AC015837	AC015837 Homo sapi
35	35.6	14.2	207259	2	AC110899	AC110899 Mus muscu
36	35.4	14.2	94739	9	AP001964	AP001964 Homo sapi
37	35.4	14.2	169091	2	AC025852	AC025852 Homo sapi
38	35.4	14.2	187372	2	AC12453	AC12453 Mus muscu
39	35.4	14.2	220470	2	AC122327	AC122327 Mus muscu
40	35.4	14.2	226366	2	AC126045	AC126045 Mus muscu
41	35.2	14.1	434	8	GMSE60	Z13956 G.max mRNA
42	35.2	14.1	9386	1	AE000791	AE000791 Borelia
43	35.2	14.1	205409	2	AC121939	AC121939 Mus muscu
44	35	14.0	46831	2	AC087204	AC087204 Homo sapi
45	35	14.0	107037	2	AF188029	AF188029 Homo sapi

#### ALIGNMENTS

RESULT 1  
AF319468  
LOCUS AF319468 406 bp mRNA linear PLN 14-DEC-2000  
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.  
ACCESSION AF319468  
VERSION AF319468.1 GI:11762085  
KEYWORDS  
SOURCE Medicago sativa.  
ORGANISM Medicago sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.  
REFERENCE  
1 (bases 1 to 406)  
Liang, J., Shah, D.M., Wu, Y.S., Rosenberger, C.A. and Hakim, S.

REFERENCE	TITLE	FEATURES
JOURNAL	Antifungal Polypeptide(s) and Methods for Controlling Plant Pathogenic Fungi	
REFERENCE	Patent: US 6121436 19-SEP-2000;	
AUTHORS	Monsanto Company; St Louis, MO	
TITLE	2 (bases 1 to 406)	
JOURNAL	Gao,A.G., Hakiml,S.M., Mltanck,C.A., Wu,Y., Woerner,B.M., Stark,D.M., Shah,D.M., Liang,J. and Rommens,C.M.	
MEDLINE	Fungal pathogen protection in potato by expression of a plant defensin peptide	
PUBMED	Nat. Biotechnol. 18 (12), 1307-1310 (2000)	
REFERENCE	3 (bases 1 to 406)	
AUTHORS	Mltanck,C.A., Wu,Y., Hakiml,S.M., Liang,J., Shah,D.M. and Gao,A.G.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway, St Louis, MO 63198, USA	
FEATURES	Location/Qualifiers	
SOURCE	1..406	
CDS	/organism="Medicago sativa"	
	/db_xref="taxon:3879"	
	75..293	
	/note="alfAFP; defensin"	
	/codon_start=1	
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	/protein_id="AAC40321.1"	
	/db_xref="GI:11762086"	
	/translation="MEKSLAGLCFLFLVFAOEIVVTEARCNELNADYKPCFSGCDTHCTTKENAVSGRCRDDEFCWCTKRC"	
	75..155	
	sig_peptide	
	mat_peptide	
	156..290	
	/product="antifungal protein"	
BASE COUNT	140 a 74 c 78 g 114 t	
ORIGIN		
Query Match	93.6%; Score 234; DB 8; Length 406;	
Best Local Similarity	100.0%; Pred. NO. 3.6e-56;	
Matches 234;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	9 CAATCATCAACAATATGAGAGAAAGAAATCACTAGCTGGCTTATGCTTCCTTGGTT 68	
DB	60 CAATCATCAACAATATGAGAGAAAGAAATCACTAGCTGGCTTATGCTTCCTTGGTT 119	
QY	69 CTCCTTGTGCACAAGAAATTTGTGGTGCAGAACCCAGAACATGTGAAATTTGGCAGAT 128	
DB	120 CTCCTTGTGCACAAGAAATTTGTGGTGCAGAACCCAGAACATGTGAAATTTGGCAGAT 179	
QY	129 AAAATATAGGGACCATGCTTTATGTTGTGTACACTCACTGCAACCAAGAGACGCA 188	
DB	180 AAAATATAGGGACCATGCTTTATGTTGTGTACACTCACTGCAACCAAGAGACGCA 239	
QY	189 GTTATGTGGAAGGTGTAGGAGCACTTCGCCGTGCTGATTAAGAATGTTAA 242	
DB	240 GTTATGTGGAAGGTGTAGGAGCACTTCGCCGTGCTGATTAAGAATGTTAA 293	
RESULT 2		
PEADRR230A	468 bp	linear
LOCUS	PEADRR230A	PLN 11-FEB-2002
DEFINITION	Pea (p1230) disease resistance response protein 230 (DRR230-a)	
ACCESSION	U01578	complete cds.
VERSION	U01578.1	GI:169073
KEYWORDS	cysteine-rich protein; disease resistance response protein 230; pathogenesis-related protein.	
SOURCE	Pisum sativum.	
ORGANISM	Pisum sativum	
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.	
REFERENCE	1 (bases 1 to 468)	
AUTHORS	Chiang,C.C. and Hadwiger,L.A.	

FEATURES	source	location/Qualifiers
TITLE	The <i>Fusarium solani</i> -induced expression of a pea gene family	
JOURNAL	Encoding high cysteine content proteins	
MOL.	Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)	
MEDLINE	92190628	
PUBMED	1799696	
COMMENT	On Feb 8, 2002 this sequence version replaced gi:247416.	
FEATURES	source	location/Qualifiers
		1..468
		/organism="Pisum sativum"
		/strain="Alaska"
		/db_xref="taxon:3888"
		/tissue_type="pod tissue treated with <i>Fusarium solani</i>
		condia"
		/dev_stage="immature"
		1..468
		/gene="DRR230-a"
		78..296
		/gene="DRR230-a"
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		/note="p1230"
		/codon_start=1
		/evidence=experimental
		/product="disease resistance response protein"
		/protein_id="AA079117.1"
		/db_xref="GI:169074"
		/translation="MEKSLACLISFLLLVLFVAOEIVSEANTCENLAGSYKGVCGFG
		CDRHCRIOEGALISCRCRDRCFCMCTKNC"
		159..293
		/gene="DRR230-a"
		/product="disease resistance response protein"
		/function="unknown"
		/note="determined by in vitro cleavage with microsomal
		membranes"
		/evidence=experimental
BASE COUNT	153 a 88 c 84 g 143 t	
ORIGIN		
Query Match	62.6%; Score 156.4; DB 8; Length 468;	
Best Local Similarity	80.0%; Pred. No. 5e-34;	
Matches	184; Conservative 0; Mismatches 46; Indels 0; Gaps 0;	
OY	13 CTAATCAACATGAGGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTGCTCTCT	72
DB	67 CTTAAGAAGCATGAGAGAAATCACTAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	126
OY	73 TTGTTGCACAGAAATTTGTGTGACAGAACGACCAACATGTGAGAAATTTGGCAGATAAT	132
DB	127 TTGTTGCACAGAAATTTGTGTGAGTGAAGCAACATGTGAGAAATTTGGCAGTTCAT	186
OY	133 ATAGGGACACATGCTTATGCTGTGTGACACTGACACCAACCAAGAGAACGACAGTTA	192
DB	187 ATAGGGAGCATGCTGCTGTGTGATGTGACCGTCACTGTGAGAACCAAGAGGGCGCAATTA	246
OY	193 GTGGAAGGTGAGGAGCAGCTTCGCGTCTGCTGTACTATAAAGATGTTAA	242
DB	247 GCGGACAGATGACGAGGATGACTTTCGCTGCTGTGCTACATAAAGACTGTTAA	296
RESULT 3		
PSPI230		
LOCUS	PSPI230	
DEFINITION	P. sativum p1230 mRNA.	
ACCESSION	X52225	
VERSION	X52225.1 GI:22208748	
KEYWORDS	secreted protein.	
SOURCE	pea.	
ORGANISM	Pisum sativum	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;	
	Pisum.	
REFERENCE	1	



[illegible]

	Query Match	Best Local Similarity	74.8%;	Score 119.4;	DB 6;	Length 494;
	Matches	Conservative	0;	Mismatches	51;	Indels
						Gaps
OY	13	CTAATCAACTATGAGAGAAATCACTAGCTGCTTATGCTTCTTCTTGGTCTCT				72
Db	35	CTAATTAAGCCATGAGAGAAATCAATAGCTGGTGTCTCTCTCTCTTCTTCACT				94
OY	73	TTGTGGACAAGAAATTTGTGTG---ACAGAAAGCAGAACATGTGAGAAATTTGGCAGATA				129
Db	95	TTGTGTCTCAAGAAAGTTGTGTGTCCAACTGAGCAGAAAGACTTTGGCAGAACTGGCTGATA				154
OY	130	AATATAGGGGACCATGCTT-----TAGTGTGTGACACTCTACTGCACCAACAAAGAGA				183
Db	155	CATACAGGGGCTCATGCTTACCACTGACACTGCATGATCACTGCAGAAACAAAGAGC				214
OY	184	ACGAGTTAGTGGAGGTGTGGGACGACCTCCGCTGGTGTGACTTAAAGATGTTATA				242
Db	215	ACTTGCTCAGACGAGATCCAGGAGCAGATTTTCCCTGTGTGGTGCACCAAAAGCTGTATA				273

RESULT	6
AB020613	
LOCUS	AB020613
DEFINITION	Vigna radiata mRNA for PDI1, complete cds.
ACCESSION	AB020613
VERSION	AB020613.1 GI:18146787
KEYWORDS	PDI1.
SOURCE	Vigna radiata (strain:B20F5 9-3-2-2) immature seed cDNA to mRNA, clone_ltr:B20 clone:pdf-1.
ORGANISM	Vigna radiata

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 Ishimoto, M. and Kaga, A.  
Mungbean defensin  
Published only in Database (2002)  
2 (bases 1 to 496)  
Ishimoto, M. and Kaga, A.  
Direct Submission  
Agricultural (01-DEC-1998) Masao Ishimoto, Chugoku National  
Agricultural Experiment Station, Laboratory of Plant Biotechnology,  
6-12-1 Nishifuketsu, Fukuyama, Hiroshima 721-6514, Japan  
(E-mail:ishimoto@cagk.affrc.go.jp, Tel:+81-849-234100(ex.231),  
Fax:+81-849-2341993)

FEATURES	source
location/Qualifiers	
1. .496	
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/db_xref="taxon:157791"	
/clone="pdf-1"	
/tissue_type="Immature seed"	
/clone_id="B20"	
1. .496	
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46. .273	
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/protein_id="DAB82453.1"	
/db_xref="GI:18146788"	
/translation="MERKSLAGLCFLFLVLAQGVVQTEAKTCENLIANTYRGPCTT TGSDCHCKNKEHRLSRGRCDRDFRCWCWTRNC"	

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BASE COUNT	148 a	104 c	106 g
ORIGIN			138 t
Query Match	45.2%	Score 113	DB 8
Best Local Similarity	73.2%	Pred. No. 1,2e-21	Length 496

Matches	175	Conservative	0	Mismatches	55	Indels	9	Gaps	2
OY	13	CTAATCAACTATGAGAGAGAAATCTAGCTGCTTATGCTTCTCTTTCTGTTCTCT	72						
Db	35	CTAATCAAGCCATGAGAGAAATCTACAGCGCGGATTTGTGTTCTCTCTCTTTCTCT	94						
OY	73	TTGTGTCACAGAAATTTGCTGCT---GATAGAGAACGACAAATGTGAGATTTGGCAGATA	129						
Db	95	TTGTGTCACAGAAATTTATGTTGTCAGACTGAGGCAAAACCTTTGGAGAACTCGCGAATA	154						
OY	130	AATATAGGGGACCATGCTT-----TATGCTGTGTACACTGACCAACCAAGAAGA	183						
Db	155	CTTACAGGGGTCATGCTTTCACCACTGGCAGCTGGAGATCACTGCAAGAAACAAAGAAC	214						
OY	184	ACGCGATTAGTGAAGAGTGTAGGGACGACCTCCGCTGGTGTTACTAAAGATGTAA	242						
Db	215	ACTTGAGGAGTGGCGAGGTGTCAGGACGATTTCCGGTGTGTTGGTGCACCTGAAAACTGTAA	273						

RESULT 7	VUSTORED	459 bp	mRNA	linear	PLN 12-SEP-1992
LOCUS	VUSTORED				
DEFINITION	Vigna unguiculata cDNA for stored cotyledon				
ACCESSION	X16877				
VERSION	X16877.1	GI:22075			
KEYWORDS					
SOURCE	Vigna radiata				
ORGANISM	Vigna radiata				

REFERENCE	1 (bases 1 to 459)
AUTHORS	Yamauchi, D.
TITLE	Direct Submission
JOURNAL	Submitted (10-OCT-1989) Yamauchi D., Dept. of Biology, Tokyo Metropolitan University, Fukuoka 2-1, Setagaya-ku, Tokyo 158, Japan
REFERENCE	2 (bases 1 to 459)
AUTHORS	Ishibashi, N., Yamauchi, D. and Minamikawa, T.
TITLE	Stored mRNA in cotyledons of <i>Vigna unguiculata</i> seeds: nucleotide sequence of cloned cDNA for a stored mRNA and induction of its synthesis by precocious germination
JOURNAL	PLANT MOL. BIOL. 15 (1), 59-64 (1990)
MEDLINE	91353865
PUBMED	21034443

FEATURES	source	Location/Qualifiers
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CDS		14..241
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BASE COUNT		136 a 99 g 133 t
ORIGIN		

[illegible]

QY	73	TTGTTGGCAGGAATTTGCT---	GACAGAGGCAGCAACATGTGAGAAATTTGGCAGATA	129
Db	63	TTGTTGCTCAAGAAAGTTTGTTGGTGCAGATGAGGCAAGACCTTGGCAGAACTGGTGATTA	122	
QY	130	AATATTAGGGGACCATGCTT-----	TACTGGTTGTGACACTGCATGCACAACCAAGAGA	183
Db	123	CATACAGGGGGTCCGTCGCTTTCACCACTGGAGGACTGGAGATGATCCTGCAGAACCAAGAAC	182	
QY	184	ACGCAAGTTAGTGGAAGGTGTAGGACACACTTCCGCTGCTGTGTACTATAAAGATGTTAA	242	
Db	183	ACTTGCTGACAGCGCAGAGGTGACGAGGATGTGTCGGTGTGGTGACACCAAGAACTGTAA	241	
RESULT 8				
PEADRR230B				
LOCUS		PEADRR230B	456 bp	mRNA
DEFINITION		Pisum sativum disease resistance response protein 39 (DRR230-b)		
ACCESSION		mRNA, complete cds.		
VERSION		L01579.88682		
KEYWORDS		L01579.1 GI:169075		
SOURCE		cysteine-rich protein; disease resistance response protein 39; pathogenesis-related protein.		
ORGANISM		Pisum sativum (strain Alaska) cDNA to mRNA.		
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.		
AUTHORS		1 (bases 1 to 456)		
TITLE		Chiang,C.C. and Hadwiger,L.A.		
JOURNAL		The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins		
MEDLINE		Wol. Plant Microbe Interact. 4 (4), 324-331 (1991)		
PUBMED		92190628		
COMMENT		On Feb 8, 2002 this sequence version replaced gi:274714.		
FEATURES		location/qualifiers		
Source		1..456		
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		/dev_stage="immature"		
gene		1..456		
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CDS		69..293		
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		/codon_start=1		
		/evidence=experimental		
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		/db_xref="GI:169076"		
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mat_peptide				
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Query Match		39.2%	Score 98;	DB 8; Length 456;
Best Local Similarity		72.1%;	Pred. No. 2.4e-17;	
Matches 173; Conservative		0;	Mismatches 55;	Indels 12; Gaps 3;
QY	15	AATCAACTATGAGCAACAATCTACTACGTGCTTATGCTTCCTCTCTTG---GTTCTC	71	

Db	60	ACTAAGTATTGAGAGAACAAATTCACCTACTGCTTGGCTTCCTCCCTCCCTGCTTC	113
QY	72	TTTGTGTGCACAGAATAATTTGTGTGCACAGAACCCAGAACATGTGAAATTTTGGCAGATAAA	131
Db	120	TTTGTGTGCACAGAATAATTTGTGTGCACAGAACCCAGAACATGTGTGAGCAATTTTGGCTGATACA	179
QY	132	TATAGGGAGCATGCTT-----TAGTGTTGTGTGACACTGCATCTGCACACCAAGAGAAC	185
Db	180	TACAGGGAGCATGCTTCCACGAATGCTATGATGTACTGTCAACAAACAAAGCGCAC	239
QY	186	GCAGTATGTGAGAGGTAGGAGCAGATCTCCGCTGCTGTGTACTGAAAAGATGTTAAAGA	245
Db	240	TTAATCAGTGGCAGCT---GCCATGACTGGAATATGTTCTGACTCAAAACTGTTAAAGA	296
RESULT 9			
LOCUS	PSPI39		
DEFINITION	P.sativum p139 mRNA.	456 bp	Linear
ACCESSION	X52224		
VERSION	X52224.1		
KEYWORDS	secreted protein.		
SOURCE	pea.		
ORGANISM	Pisum sativum		
REFERENCE	1		
AUTHORS	Chiang, C. C. and Hadwiger, L. A.		
TITLE	The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins		
JOURNAL	Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)		
MEDLINE	92190628		
REFERENCE	2 (bases 1 to 456)		
AUTHORS	Chiang, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-AUG-1990) Chiang C., Washington State University, Dept. of Plant Pathology, Pullman, WA 99164-6430, USA		
FEATURES	Location/Qualifiers		
source	1..456		
gene	/organism="Pisum sativum"		
CDs	/db_xref="taxon:3888"		
	/tissue_type="endocarp"		
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	/gene="p139"		
	/codon_start=1		
	/protein_id="CA36473.1"		
	/db_xref="GI:22208745"		
	/translation="MEKSLAALFSLFLVLYFAQDEIVTEANTCEHLADTYRQVCFT"		
	NASODDHCKNKAHLISGCHMKPCFQNC"		
sig_peptide	69..152		
	/gene="p139"		
mat_peptide	153..290		
	/gene="p139"		
	/product="unnamed"		
BASE COUNT	155 a 81 c 79 g 141 t		
ORIGIN			
Query Match	39.2%;	Score 98;	DB 8; Length 456;
Best Local Similarity	72.1%;	Pred. No. 2.4e-17;	
Matches 173:	Conservative	0;	Mismatches 55; Indels 12; Gaps 3;
QY	15	AATCAACTATGAGAGAGAATCTACTAGCTGCTTATGCTTCCTCTTCTG---GTTCTC	71
Db	60	ACTAAGTATTGAGAGAACAAATTCACCTACTGCTTGTCTTCCTCTCTCTGTTCTC	119
QY	72	TTTGTGTGCACAGAATAATTTGTGTGCACAGAACCCAGAACATGTGAAATTTTGGCAGATAAA	131
Db	120	TTTGTGTGCACAGAATAATTTGTGTGCACAGAACCCAGAACATGTGTGAGCAATTTTGGCTGATACA	179



**D**

QY Db	<div style="width: 100px; height: 100px; background-color: #f0f0f0; margin: auto;"></div>	108 ACATGTGAGATTTCGCAGATAAATATPAGGGACCATCCTTAACTGGT-----TGTCAC 161                -   -   -                  -   -   -   4 ACTTTGGCGAGAACCTTTCTGGAACCTTCCAGGAGACCATTGCACTTCAGATGCAACTGCCAAC 63
----------	---	--

Query Match	16.0%	Score 40:	DB 6:	Length 141:
Best Local Similarity	60.6%	Pred. No.	0.92:	
Matches 83; Conservative	0;	Mismatches	48;	Indels 6; Gaps 1;



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 06:14:34 ; Search time 931.765 Seconds  
(without alignments)  
695.261 Million cell updates/sec

Title: US-10-010-731-14  
Perfect score: 244  
Sequence: 1 ATCCN1ANTYRGPCFGCGDCHCKTKEHLISGRCDPRFC 40

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n model -DEY=xlh  
-O/cgn2\_1/USFTO.spool/US10010731/runat\_17062003\_095705\_2817/app\_query.fasta.1.398  
-DB=EST -OPM=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USFR-US10010731.ecgn.1.1.2463.etrnat.17062003.095705.28171 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEIOBURY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estlom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vtl:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	185	75.8	446 9	AJ498901
2	184	75.4	426 12	BG838678
3	181	74.2	487 13	B1321179
4	162	66.4	517 9	AJ308155
5	145.5	59.6	574 14	B0151477
6	132.5	54.3	503 12	BF633403
7	118	48.4	438 13	B1642738
8	116	47.5	366 13	B1321308
9	77	31.6	238 13	B1642792
10	76.5	31.4	1087 17	CNS05E63
11	75.5	30.9	369 9	AJ499268
12	74.5	30.5	528 12	BE942973
13	74.5	30.5	548 9	AL367974
14	74.5	30.5	548 10	AM585761
15	74.5	30.5	596 12	BF645101
16	74.5	30.5	605 12	BF649943
17	74.5	30.5	650 12	BF647513
18	74.5	30.5	654 12	BF645260
19	74.5	30.5	658 12	BF649855
20	74.5	30.5	662 12	BF650421
21	73.5	30.1	217 14	T09323
22	72.5	29.7	261 9	AJ499675
23	72.5	29.7	262 9	AJ500483
24	72.5	29.7	292 10	AM203222
25	72.5	29.7	360 9	AJ474240
26	72.5	29.7	369 9	AJ499336
27	72.5	29.7	379 9	AJ499347
28	72.5	29.7	373 9	AJ499760
29	72.5	29.7	378 9	AJ502212
30	72.5	29.7	384 9	AJ500150
31	72.5	29.7	385 9	AJ500594
32	72.5	29.7	386 9	AJ500674
33	72.5	29.7	418 10	AV721256
34	72.5	29.7	420 9	AJ474375
35	72.5	29.7	420 9	AJ474376
36	72.5	29.7	424 14	B0661645
37	72.5	29.7	427 13	BM369664
38	72.5	29.7	427 13	BM377547
39	72.5	29.7	442 9	AJ499945
40	72.5	29.7	449 9	AJ499841
41	72.5	29.7	450 9	AJ499952
42	72.5	29.7	451 13	BM369646
43	72.5	29.7	454 9	AJ500390
44	72.5	29.7	458 9	AL383916
45	72.5	29.7	463 9	AJ499925

## ALIGNMENTS

RESULT 1  
LOCUS AJ498901  
DEFINITION AJ498901 MYPOSE Medicago truncatula cDNA clone mt--acc955209h10,  
mRNA sequence.  
ACCESSION AJ498901  
VERSION AJ498901.1 GI:22089344  
KEYWORDS  
SOURCE  
ORGANISM Medicago truncatula  
bairrel medic.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.  
REFERENCE  
1 (bases 1 to 446)









US-10-010-731-14 (1-40) x B1642738 (1-438)

OY 1 AlAtHrCysGluAsnLeuAlaAsnTrHrYrGlyProCysPhe-----GlyGlyCys 18  
|||||  
DB 123 GCGACTTGTGAGAACCTGGCTGCTACATTCAGGGGCTGTATGCATTCACCTCTGCTACCTGC 182  
|||||

OY 19 AspPheHicCysLysTrHrYrGluHisLeuLeuSerGlyArGcYsArGAspAspPheArG 38  
|||||  
DB 183 GACGATCATCGACATGTCNN-NNACACTTACTAGTGGCAGGTGCAGACAGCATGTCCG 241  
|||||

RESULT 8  
LOCUS B1321308  
DEFINITION B1321308 366 bp mRNA linear EST 29-NOV-2001  
ID: GM-c1077-2037 5', similar to SW:10KRD\_VIGUN P18646 10 KD PROTEIN  
PRECURSOR: mRNA sequence.

ACCESSION B1321308  
VERSION B1321308.1 GI:15000494  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 366)  
Shoemaker,R., Klein,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna  
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wille,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk  
R., Rilter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: cu@resgen.com  
Seq primer: -40RP from Gibco  
High quality sequence stop: 343.  
Location/Qualifiers  
1..366  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: GM-c1077-2037"  
/clone\_lib="GM-c1077"  
/tissue\_type="18 day old 'Williams' seedlings"  
/dev\_stage="18 day old 'Williams' seedlings"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site.1: EcoRI; Site.2:  
XhoI. The mRNA was isolated from cotyledons of 18-day-old  
'Williams' seedlings which were greenhouse grown in  
potting soil. The cotyledons were flash-frozen in liquid  
nitrogen. Stratagene's cDNA Synthesis Kit (catalog number  
200401) was used to synthesize the cDNA. First-strand  
synthesis was performed with 5-methyl dCTP, hence the  
ligated cDNA was hemimethylated. A modification of  
Stratagene's first-strand synthesis primer was used. An  
'anchor' nucleotide (V=A, C, or G) was added to the 3' end  
of the primer (GAGAGAGAGAGAGAGAGACTGCTCGAG(T)18V) to  
anchor the primer at the 5' end of the poly(A) tract.  
After second-strand synthesis, the cDNA ends were filled  
in with cloned Pfu DNA, ligated to EcoRI adapters and  
subsequently phosphorylated. The cDNA was then  
precipitated and redissolved in sterile, RNase-  
free water. The XhoI site within the first-strand

synthesis primer was then restricted by digestion with  
XhoI from Promega (400/ul); all XhoI sites in the cDNA  
would be protected by their hemimethylated status. The  
cDNA constructs were size-fractionated with a 500bp  
cutoff, using Sephacryl S-500 High Resolution (Pharmacia  
Biotech) in a 2-mm diameter column and a bed volume of  
approximately 1ml. The column eluent was precipitated,  
redissolved, and ligated into Stratagene's pBluescript II  
XR predigested vector (pBluescript II SK(+)) vector that  
has been digested with EcoRI and XhoI, and phosphorylated  
by Stratagene). This library was constructed in the  
Laboratory of Dr. Paul Keim and Dr. Virginia H. Corryell at  
Northern Arizona University."

BASE COUNT 124 a 60 c 70 g 112 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3,8e-06 Length: 366  
Score: 116.00 Matches: 19  
Percent Similarity: 86.36% Conservative: 0  
Best Local Similarity: 86.36% Mismatches: 3  
Query Match: 47.54% Indels: 0  
DB: 13 Gaps: 0

US-10-010-731-14 (1-40) x B1321308 (1-366)

OY 18 CysAspPheHicCysLysTrHrYrGluHisLeuLeuSerGlyArGcYsArGAspAspPhe 37  
|||||  
DB 5 TCGGATGATCATCGACAAAGACAGACTTCTCAGAGACAGATGCAGGAGCATTTT 64  
|||||

OY 38 ArGcYs 39  
|||||

DB 65 CGCTGT 70

RESULT 9  
LOCUS B1642792  
DEFINITION B1642792 238 bp mRNA linear EST 10-SEP-2001  
TSS1220 TZS (Sapwood-heartwood transition zone of black locust -  
Summer) Robinia pseudocacia cDNA, mRNA sequence.

ACCESSION B1642792  
VERSION B1642792.1 GI:15545002  
KEYWORDS EST.  
SOURCE Robinia pseudocacia.  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Robiniae;  
Robinia.  
1 (bases 1 to 238)  
Han,K.-H., Yang,J., Park,S., Paule,C.R., Kapur,V., Retzel,E.F.,  
Kandem,D.P. and Keathley,D.E.  
Analysis of gene expression patterns in trunk wood of a mature  
black locust (Robinia pseudocacia)  
Unpublished (2002)  
Contact: Kyung-Hwan Han  
Department of Forestry  
Michigan State University  
126 Natural Resources, East Lansing, MI 48824-1222, USA  
Tel: 517 353 4751  
Fax: 517 432 1143  
Email: hanky@msu.edu.  
Location/Qualifiers  
1..238  
/organism="Robinia pseudocacia"  
/db\_xref="taxon:35938"  
/clone\_lib="TZS (Sapwood-heartwood transition zone of  
black locust - Summer)"  
/tissue\_type="sapwood-heartwood transition zone"  
/dev\_stage="mature tree"  
/note="Vector: lambda Triplex; Site.1: Sfi IA; Site.2: Sfi  
IB. The cDNA library was made from the sapwood-heartwood  
transition zone of a mature black locust tree collected in  
Michigan in late July."

BASE COUNT	63 a	60 c	49 g	60 t	6 others
ORIGIN					
Alignment Scores:					
Pred. No.:	0.483	Length:	238		
Score:	77.00	Matches:	19		
Percent Similarity:	58.33%	Conservative:	2		
Best Local Similarity:	52.78%	Mismatches:	12		
Query Match:	31.56%	Indels:	3		
Db:	13	Gaps:	1		
US-10-010-731-14 (1-40) x B1642792 (1-238)					
Oy	1 AlatrthrycsgjuanslenuAlaasnthrytarnglyprocysphe-----glyglycys 18				
Db	132 TCGACTTCGGAACCTGGCTGTACATTCAGGGGCTTATCATCACCTGTGTCTACCTGC 191				
Oy	19 AsphenHtCys-LysthrylgjuHtIsleuIeuserclyargcys 33				
Db	192 GACGATCATCTCGNNGACATATATATCTTACTCTAGTCCACAGTTC 237				
RESULT 10					
CNS05E63	1087 bp DNA linear GSS 26-MAY-2000				
LOCUS	Tetradodon nigroviridis genome survey sequence T7 end of clone				
DEFINITION	017C04 of library A from Tetradodon nigroviridis, genomic survey				
ACCESSION	AL333300.1 GI:8227058				
VERSION	GSS: genome survey sequence.				
KEYWORDS	Tetradodon nigroviridis.				
SOURCE	Tetradodon nigroviridis.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradodon.				
REFERENCE	1 (bases 1 to 1087)				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.				
TITLE	Human gene number estimate provided by genome wide analysis using Tetradodon nigroviridis DNA sequence				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1087)				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Fitzmes,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 1087)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-APR-2000)				
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetradodon">http://www.genoscope.cns.fr/Tetradodon</a> .				
FEATURES	Location/Qualifiers				
source	1..1087				
	/organism="Tetradodon nigroviridis"				
	/db_xref="taxon:99883"				
	/clone="017C04"				
	/clone_id="A"				
	/note="Genoscope sequence ID: C0NA017B802C1-end : T7"				
BASE COUNT	301 a	231 c	276 g	266 t	13 others
ORIGIN					
Alignment Scores:					
Pred. No.:	4.16	Length:	1087		
Score:	76.50	Matches:	3		
Percent Similarity:	45.24%	Conservative:	16		
Best Local Similarity:	38.10%	Mismatches:	14		

Query Match:	31.35%	Indels:	9
DB:	17	Gaps:	2
US-10-010-731-14 (1-40) x CNS05E63 (1-1087)			
OY	4 GluusInleuAlaAsnTrpTyrArgGlProCys-----PheGlyIcys	18 	
Db	880 GAGTTNMGCCGNACAACTACAGAGCACTTGTAAGGTCTGAACGGGTATGATGCGGTCT	939 	
OY	19 AspRheHiscLysThrLysGlnHisLeuLeuSerGlyArgCysArGAspRhpAarg	38 	
Db	940 ACTTAACAACACACACACACACACAGTCACACAGAGAATAATGT-----TCA	987    :::>:::    ::	
OY	39 CysCys	40 	
Db	988 TGTTCG	993	
RESULT 11			
LOCUS	AJ499268	369 bp	mRNA linear EST 09-AUG-2002
DEFINITION	AJ499268 MTGM Medicago truncatula cDNA clone mtgmacc120002b01,		
ACCESSION	AJ499268		
VERSION	AJ499268.1		
KEYWORDS	GI:22089711		
SOURCE	EST.		
ORGANISM	'barrel medic. Medicago truncatula		
REFERENCE	1 (bases 1 to 369) Krajinski,F., Montney,K., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T., Linke,B., Franken,P., Kuester,H., Perlick,A.M. and Puehler,A.		
TITLE	Detection of transcript sequences from mycorrhizal roots of the model mycorrhiza Medicago truncatula genotype A17 - Glomus intracellular using the approach of an EST genome project based on an SSH library		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Krajinski F IG Molekulargenetik Herrenhaeuser Str. 2 D-30419 Hannover, Germany.		
FEATURES	Location/Qualifiers		
source	1..369 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="mtgmacc120002b01" /clone_id="MTGM" /lssne_type="mycorrhizal roots" /dev_stage="3 weeks after inoculation" /note="Vector: pGEM-Teasy; genotype A17; cDNA was prepared from total RNA using the SMART PCR cDNA system (Clontech) from roots harvested three weeks after inoculation with Glomus intraradices. This cDNA was used as tester in a Suppression Subtractive Hybridization (SSH). The SSH-cDNA fragments were generated using the SSH-adaptor sequences ctaatagactcaataaggcgacgagcgccgcggccgacagt and ctaatagactcaataaggcgacgagcgccgcggccgacagt (Clontech) and ligated after suppression subtractive hybridization in to the pGBM-Teasy vector from Promega. Plasmids containing cDNA inserts were propagated in E. coli TOP 10F' cells (Invitrogen)"		
BASE COUNT	125 a	53 c	69 g 122 t
ORIGIN			
Alignment Scores:			
Pred. No.:	1.38	Length:	369
Score:	75.50	Matches:	15
Percent Similarity:	45.24%	Conservative:	4
Best local Similarity:	35.71%	Mismatches:	18
Query Match:	30.94%	Indels:	5
DB:	9	Gaps:	2



Best Local Similarity: 38.10% Mismatches: 19  
 Query Match: 30.53% Indels: 5  
 DB: 9 Gaps: 2  
 US-10-010-731-14 (1-40) x AL367974 (1-548)

QY 3 CysGluAsnLeuAlaSnhrTYrArgGlyProCysPhe-----GlyGlyCysaspPhe 20  
 ||||| : : ||||| ||||| ||||| |||||  
 Db 287 TGTGAAGGCGGAGCAAAACATGTCGACCTTGTCTATCTCAGGAATTTGTAAGA 228

QY 21 HisCysIsthrLysGluHisLeuSerGlyArgCysArgaspPhe-----Phe 37  
 ||||| ||||| ||||| ||||| ||||| |||||  
 Db 227 CAGTCATCAATGTTGAGCATGCAACTTGTGTCCTTGTCCACCGTCAGGCAATTTGTTT 168

QY 38 ArgCys 39  
 |||||  
 Db 167 GCCTGC 162

RESULT 14  
 AM585761 548 bp mRNA linear EST 07-SEP-2000  
 LOCUS EST317384 MHAM Medicago truncatula/Gloms versiforme mixed EST  
 DEFINITION library cDNA clone pMHAM-39M12, mRNA sequence.  
 ACCESSION AM585761 GI:7265275  
 VERSION AM585761.1  
 KEYWORDS EST.  
 SOURCE Medicago truncatula/Gloms versiforme mixed EST library.  
 ORGANISM Eukaryota; mixed EST libraries.  
 REFERENCE 1 (bases 1 to 548)  
 AUTHORS Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,  
 Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.  
 TITLE ESTs from roots of Medicago truncatula after colonization with  
 Gloms versiforme  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Maria J. Harrison  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73401, USA  
 Tel: 580-223-5810  
 Fax: 580-221-7380  
 Email: mjharrison@noble.org  
 Noble EST name: N254689e  
 TIGR sequence name: MDAF78TK  
 More information is available at: 'http://chrysis.tamu.edu/medicago/'  
 Seq primer: Skmod (CTA gAA CTA gtg. gat CC).  
 Location/Qualifiers  
 1..348  
 /organism="Medicago truncatula/Gloms versiforme mixed EST  
 library"  
 /cultivar="Medicago truncatula genotype Al7"  
 /db\_xref="taxon:119092"  
 /clone="pMHAM-39M12"  
 /tissue\_type="MHAM"  
 /tissue\_type="roots colonized with Gloms versiforme"  
 /dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days  
 post-inoculation with Gloms versiforme. The library was  
 made from a mixture of RNA from each of these stages."  
 /lab\_host="E. coli strain XLOLR"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA from  
 roots harvested at 10, 17, 22, 31 and 38 days  
 post-inoculation with Gloms versiforme. The cDNA was  
 directionally ligated into the unzip XR vector from  
 Stratagene and packaged using GigaPack III Gold packaging  
 extracts. Plasmids containing cDNA inserts were excised  
 from the recombinant lambda-Zap phage using Ex-assist  
 helper phage and propagated in XLOLR cells."

BASE COUNT 169 a 101 c 99 g 179 t  
 ORIGIN  
 Alignment Scores:

Pred. No.: 3.18 Length: 548  
 Score: 74.50 Matches: 16  
 Percent Similarity: 42.86% Conservative: 2  
 Best Local Similarity: 38.10% Mismatches: 19  
 Query Match: 30.53% Indels: 5  
 DB: 10 Gaps: 2  
 US-10-010-731-14 (1-40) x AM585761 (1-548)

QY 3 CysGluAsnLeuAlaSnhrTYrArgGlyProCysPhe-----GlyGlyCysaspPhe 20  
 ||||| : : ||||| ||||| ||||| |||||  
 Db 273 TGTGAAGGCGGAGCAAAACATGTCGACCTTGTCTATCTCAGGAATTTGTAAGA 332

QY 21 HisCysIsthrLysGluHisLeuSerGlyArgCysArgaspPhe-----Phe 37  
 ||||| ||||| ||||| ||||| ||||| |||||  
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 VERSION BF645101.1  
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 REFERENCE 1 (bases 1 to 596)  
 AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Iman,J.T., Weller,J.W. and May,G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -  
 Center for Medicago Genomics Research  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Dixon RA  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7302  
 Fax: 580 221 7380  
 Email: radixon@noble.org  
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Job time : 934.765 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 06:15:24 ; Search time 31.5294 Seconds  
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389.068 Million cell updates/sec

Title: US-10-010-731-14

Perfect score: 244

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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13	185	75.8	507	4	US-09-003-198A-10	Sequence 10, Appl
14	185	75.8	507	4	US-09-428-805-10	Sequence 9, Appl
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16	171	70.1	327	4	US-09-003-198A-9	Sequence 9, Appl
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28	62	25.4	150	1	US-08-377-687-31	Sequence 31, Appl
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36	58	23.8	1356	4	US-09-134-001C-617	Sequence 17, App
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#### ALIGNMENTS

RESULT 1  
US-08-766-355-6  
Sequence 6, Application US/08766355  
Patent No. 6121436  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakimi, Salim  
TITLE OF INVENTION: Antifungal polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
zip: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,355  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577

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: INFORMATION FOR SEQ ID NO: 6:
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:   TYPE: nucleic acid
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:   NAME/KEY: modified_base
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: RESULT 2
: US-09-003-198A-6
: Sequence 6, Application US/09003198A
: Patent No. 6316407
: GENERAL INFORMATION:
:   APPLICANT: Liang, Jihong
:   APPLICANT: Shah, Dilip Meganalal
:   APPLICANT: Wu, Yonie S.
:   APPLICANT: Rosenberger, Cindy A.
:   APPLICANT: Hakimi, Salim
:   TITLE OF INVENTION: Antifungal Polypeptide and Methods for
:   NUMBER OF SEQUENCES: 19
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Arnold White & Durkee
:     STREET: P.O. Box 4433
:     CITY: Houston
:     STATE: Texas
:     COUNTRY: USA
:     ZIP: 77210
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     OPERATING SYSTEM: IBM PC compatible
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:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/003,198A
:     FILING DATE: 07-JAN-1998
:   CLASSIFICATION:
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Paterson, Melinda L.
:       REGISTRATION NUMBER: 33,062
:       TELECOMMUNICATION INFORMATION:
:         TELEPHONE: (713) 787-1400
:         TELEFAX: (713) 787-1440
:       INFORMATION FOR SEQ ID NO: 6:
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: US-09-428-805-6
: Sequence 6, Application US/09428805
: Patent No. 6329504
: GENERAL INFORMATION:
:   APPLICANT: Liang, Jihong
:   APPLICANT: Shah, Dilip Meganalal
:   APPLICANT: Wu, Yonie S.
:   APPLICANT: Rosenberger, Cindy A.
:   APPLICANT: Hakimi, Salim
:   TITLE OF INVENTION: Antifungal Polypeptide and Methods for
:   NUMBER OF SEQUENCES: 14
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Arnold, White & Durkee
:     STREET: P.O. Box 77210
:     CITY: Houston
:     STATE: Texas
:     COUNTRY: United States of America
:     ZIP: 77210
:   COMPUTER READABLE FORM:
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:     FILING DATE:
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:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: 08/766,355
:     FILING DATE:
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Kitchell, Barbara S.
:       REGISTRATION NUMBER: 33,928
:       TELECOMMUNICATION INFORMATION:
:         TELEPHONE: (512) 418-3000
:         TELEFAX: (512) 474-7577
:       INFORMATION FOR SEQ ID NO: 6:
:         SEQUENCE CHARACTERISTICS:
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US-09-428-805-6

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; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Meganalal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 18:
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; Sequence 5, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Meganalal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,355
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
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: Sequence 5, Application US/09003198A

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RESULT 6
US-09-003-198A-5
Sequence 5, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOST:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURES:
NAME/KEY: modified_base
LOCATION: 17
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US-09-003-198A-5
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Db       83 ACATGTGCAGAAATTTGGCAGATAAATATAGGGACCATGCTTAGTGCGTTGTGACACTCAC 142
QY       22 CyslStThllyGlnHisleueusercilyArGcyArsArgasparsPhearGcyScys 40
| | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db       143 TGCAACAACCAGAAGACGCAGATTAGTGAAGGTGTAGGGACCACTTCGCCGTCCTGC 199

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APPLICATION NUMBER: US/09/428,805  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/766,355  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-428-805-13

Alignment Scores:  
Pred. No.: 1.94e-17 Length: 250  
Score: 185.00 Matches: 30  
Percent Similarity: 86.84% Conservative: 3  
Best Local Similarity: 78.95% Mismatches: 5  
Query Match: 75.82% Indels: 0  
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-428-805-13 (1-250)

QY 2 Thrcysgluasnlleuilaasnthrttyrarglyprocysphcglycysasrphnehs 21  
|||||  
Db 108 ACATGTGAGAAATTGGCAGATAATATAGGGACCATGCTTTAGTGTGTGACACTCAC 167

QY 22 CysLysThrLysgluHsleuLeuSerGlyArgCysArgAspAspPheArgCys 39  
||| |||||  
Db 168 TGCACAACCAAGAGAACGACGTTAGTGAAGCTGTAGGACGACACTCCGCTGC 221

## RESULT 11

US-09-003-198A-19  
Sequence 19, Application US/09003198A

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakiml, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
OPERATING SYSTEM: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,198A  
FILING DATE: 07-JAN-1998  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT:193  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 490 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-003-198A-19

Alignment Scores:  
Pred. No.: 4.54e-17 Length: 490  
Score: 185.00 Matches: 30  
Percent Similarity: 86.84% Conservative: 3  
Best Local Similarity: 78.95% Mismatches: 5  
Query Match: 75.82% Indels: 0  
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-003-198A-19 (1-490)

QY 2 Thrcysgluasnlleuilaasnthrttyrarglyprocysphcglycysasrphnehs 21  
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Db 159 ACATGTGAGAAATTGGCAGATAATATAGGGACCATGCTTTAGTGTGTGACACTCAC 218

QY 22 CysLysThrLysgluHsleuLeuSerGlyArgCysArgAspAspPheArgCys 39  
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Db 219 TGCACAACCAAGAGAACGACGTTAGTGAAGCTGTAGGACGACACTCCGCTGC 272

## RESULT 12

US-08-766-355-10  
Sequence 10, Application US/08766355

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakiml, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
OPERATING SYSTEM: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,355  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 507 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: one-of(17, 424, 485)



Query Match: 75.82% Indels: 0  
DB: 4 Gaps: 0

US-10-010-731-14 (1-40) x US-09-428-805-10 (1-507)

QY 2 ThcGcGluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyCysAspPheHis 21  
|||||  
DB 176 ACATGTGAGAAATTGGCAGATAATATAGGGACCATGCTTGTGTTGTGACACCTCAC 235  
|||||

QY 22 CysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39  
|||  
DB 236 TGCACACACAGAACGACGATTAGTGGAGGTGAGGACGACTTCGCTGC 289  
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RESULT 15

US-08-766-355-9  
; Sequence 9, Application US/08766355  
; Patent No. 6121436

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip Maganlal

; APPLICANT: Wu, Yoonie S.

; APPLICANT: Rosenberger, Cindy A.

; APPLICANT: Hakiml, Salim

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; NUMBER OF INVENTION: Controlling Plant Pathogenic Fungi

; CORRESPONDENCE ADDRESSES: 14

; ADDRESS: Arnold, White & Durkee

; STREET: P.O. Box 77210

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,355

; FILING DATE: Concurrently Herewith

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: MOBT:063

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 327 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: one-of(244, 305)

; OTHER INFORMATION: /mod\_base= OTHER

; OTHER INFORMATION: /note= "N = A or C or G or T"

US-08-766-355-9

Alignment Scores:

Pred. No.: 2.34e-15

Score: 171.00

Percent Similarity: 86.11%

Best Local Similarity: 77.78%

Query Match: 70.08%

DB: 3

length: 327  
Matches: 28  
Conservative: 3  
Mismatch: 5  
Indels: 0  
Gaps: 0

US-10-010-731-14 (1-40) x US-08-766-355-9 (1-327)

QY 4 GluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyCysAspPheHisCysLys 23

DB 1 GAGAAATTTGGCGGATAGTATAGCGGACCATGCTTGTGTTGTGACACTCCTCAC 60  
|||||

QY 24 ThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39  
|||||

DB 61 ACCAAGAGAGAACGCGAGTTAGTGAAGGTGAGGATGACTTTCGTTGT 108  
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Search completed: June 21, 2003, 07:53:54  
Job time : 36.5294 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 07:19:24 ; Search time 97.8824 Seconds  
(without alignments)  
599.670 Million cell updates/sec

Title: US-10-010-731-14

Perfect score: 244  
Sequence: 1 ATCENMANTYRRCPCFGCDHFCKTKEHLISGRCDRFRCC 40

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Zgapop 6.0, Zgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO/spool/US10010731/runat\_17062003\_095706\_28273/app.query.fasta\_1.398  
-DB=PubMed\_Applications\_NA -QFWT=fastcap -SUFFIX=trpb -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USFR=US10010731.ecgn\_1.1.71 &runat\_17062003\_095706\_28273  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications\_NA:\*

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4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	244	100.0	293	9	US-10-010-731-6
2	199	81.6	461	9	US-10-178-213-451
3	194	79.5	189	9	US-10-010-731-18
4	194	79.5	200	9	US-10-010-731-5

5	190	77.9	494	9	US-09-805-694B-5	Sequence 5, Appl1
6	185	75.8	250	9	US-10-010-731-13	Sequence 13, Appl1
7	185	75.8	490	9	US-10-010-731-19	Sequence 19, Appl1
8	185	75.8	507	9	US-10-010-731-10	Sequence 10, Appl1
9	183.5	75.2	420	9	US-10-178-213-436	Sequence 436, App
10	183	75.0	563	9	US-10-178-213-439	Sequence 439, App
11	171	70.1	327	9	US-10-010-731-9	Sequence 9, Appl1
12	162	66.4	141	10	US-09-759-584-35	Sequence 35, Appl1
13	140	57.4	464	9	US-10-178-213-379	Sequence 379, App
14	85.5	35.0	471	9	US-10-178-213-100	Sequence 100, App
15	80.5	33.0	441	9	US-10-178-213-106	Sequence 106, App
16	80	32.8	534	9	US-10-178-213-103	Sequence 103, App
17	75	30.7	468	9	US-10-178-213-97	Sequence 97, Appl
18	72.5	29.7	553	9	US-10-178-213-340	Sequence 340, App
19	72	29.5	573	9	US-10-178-213-403	Sequence 403, App
20	71.5	29.3	260	10	US-09-878-574-13068	Sequence 13068, A
21	71.5	29.3	272	10	US-09-878-574-10791	Sequence 10791, A
22	71.5	29.3	277	10	US-09-878-574-11794	Sequence 11794, A
23	71.5	29.3	361	10	US-09-878-574-1139	Sequence 1139, Ap
24	71.5	29.3	445	9	US-10-178-213-343	Sequence 343, App
25	71.5	29.3	459	9	US-10-178-213-334	Sequence 334, App
26	71.5	29.3	2146	10	US-09-954-456-527	Sequence 527, App
27	71.5	29.3	2146	10	US-09-842-307-1	Sequence 1, Appl1
28	70.5	28.9	425	9	US-10-178-213-325	Sequence 325, App
29	70.5	28.9	587	9	US-10-178-213-331	Sequence 331, App
30	69.5	28.5	275	10	US-09-878-574-14296	Sequence 14296, A
31	69.5	28.5	466	9	US-10-178-213-385	Sequence 385, App
32	68.5	28.1	243	10	US-09-878-574-13309	Sequence 13309, A
33	67.5	27.7	246	10	US-09-878-574-12979	Sequence 12979, A
34	67.5	27.7	246	10	US-09-878-574-15260	Sequence 15260, A
35	67.5	27.3	257	10	US-09-878-574-13340	Sequence 13340, A
36	66.5	27.3	264	10	US-09-878-574-13620	Sequence 13620, A
37	66.5	27.3	338	9	US-10-178-213-427	Sequence 427, App
38	66.5	27.3	504	9	US-10-178-213-409	Sequence 409, App
39	66.5	27.3	635	9	US-10-178-213-37	Sequence 37, Appl
40	65	26.6	73308	10	US-09-954-456-2276	Sequence 2276, Ap
41	64	26.2	373	10	US-09-770-696-283	Sequence 283, App
42	64	26.2	1633	10	US-09-070-927A-254	Sequence 254, App
43	63.5	26.0	1399	9	US-10-178-213-337	Sequence 337, App
44	63.5	26.0	17996	10	US-09-764-887-2695	Sequence 2695, Ap
45	63	25.8	347	10	US-09-864-761-19530	Sequence 19530, A

#### ALIGNMENTS

RESULT 1  
US-10-010-731-6  
; Sequence 6, Application US/10010731  
; Publication No. US20030041347A1  
; GENERAL INFORMATION:

APPLICANT: Liang, Jihong  
Shah, Dilip Meghmal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010.731

FILING DATE: 13-NO. US20030041347A1-2001

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/003,198
  FILING DATE: 07-JAN-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: Patterson, Melinda L.
    REGISTRATION NUMBER: 33,062
    REFERENCE/DOCKET NUMBER: MOBT:193
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (713) 787-1400
    TELEFAX: (713) 787-1440
  INFORMATION FOR SEQ ID NO: 6:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 293 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
  FEATURE:
    NAME/KEY: modified_base
    LOCATION: one-of(17, 265)
    OTHER INFORMATION: /mod_base= OTHER
    /note= "N = A or C or G or T"
  SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-010-731-6

Alignment Scores:
Pred. No.: 7,54e-28 Length: 293
Score: 244.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-6 (1-293)

QY 1 AlaThcYgSLuAsnleuAlaSnThrTYrArgGLyProCysPheGLyCysaspHe 20
    |||||||
DB 173 GCTACTGTGAGAAATTGGCTACATACAGGGGACACAGCTTCGCTGCTGACTTT 232
    |||||||
QY 21 HtScYsLysThrLysGLuHtSLeulSerGLyArGcYsArGAspPheArGcYs 40
    |||||||
DB 233 CACTGCAAAACCAAGACACTTACTTAGCGGAGGTGCAGGACGACTTCCGCTGCTGC 292
    |||||||

RESULT 2
US-10-178-213-451.
  Sequence 451, Application US/10178213
  Publication No. US20030041348A1
  GENERAL INFORMATION:
    APPLICANT: Simmons, Carl R.
    APPLICANT: Navarro Acevedo, Pedro A.
    APPLICANT: Harvell, Leslie
    APPLICANT: Cahoon, Rebecca
    APPLICANT: McCutchen, Billy Fred
    APPLICANT: Lu, Albert
    APPLICANT: Herrmann, Rafael
    APPLICANT: Wong, James
  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
  TITLE OF INVENTION: Use
  FILE REFERENCE: 35718/246703
  CURRENT APPLICATION NUMBER: US/10/178,213
  FILING DATE: 2002-06-21
  PRIOR APPLICATION NUMBER: 60/300,152
  PRIOR FILING DATE: 2001-06-22
  PRIOR APPLICATION NUMBER: 60/300,241
  PRIOR FILING DATE: 2001-06-22
  NUMBER OF SEQ ID NOS: 469
  SOFTWARE: FastSeq for Windows Version 4.0
  SEQ ID NO 451
  LENGTH: 461
  TYPE: DNA
  ORGANISM: Arabidopsis hypogaea
  FEATURE:
    NAME/KEY: CDS
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LOCATION: (44)...(271)
FEATURE:
  NAME/KEY: mat.peptide
  LOCATION: (128)...(268)
FEATURE:
  NAME/KEY: misc.feature
  LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
  OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451

Alignment Scores:
Pred. No.: 7,31e-21 Length: 461
Score: 199.00 Matches: 35
Percent Similarity: 87.80% Conservative: 1
Best Local Similarity: 85.37% Mismatches: 3
Query Match: 81.56% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-10-178-213-451 (1-461)

QY 1 AlaThcYgSLuAsnleuAlaSnThrTYrArgGLyProCysPhe-----GLyGLyCys 18
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DB 128 GCACGCTGTGAGAACCTGGCGGATACCTACAGGGGACATGCTTACACACCGAAGCTGC 187
    |||||||
QY 19 AspPheHtScYsLysThrLysGLuHtSLeulSerGLyArGcYsArGAspPheArG 38
    |||||||
DB 188 GCAGCACCAGCTGCAAGAAACAGGACACCTGCTCAGGGCGCGCTGCCGACGACTTCCGC 247
    |||||||
QY 39 Cys 39
DB 248 TGT 250

RESULT 3
US-10-010-731-18
  Sequence 18, Application US/10010731
  Publication No. US20030041347A1
  GENERAL INFORMATION:
    APPLICANT: Liang, Jihong
    APPLICANT: Wu, Yonnie S.
    APPLICANT: Rosenberger, Cindy A.
    APPLICANT: Hakimi, Salim
  TITLE OF INVENTION: Antifungal Polypeptide and Methods for
  TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
  NUMBER OF SEQUENCES: 19
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: Texas
    COUNTRY: USA
    ZIP: 77210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/010,731
    FILING DATE: 13-NO. US20030041347A1-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/003,198
    FILING DATE: 07-JAN-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: Patterson, Melinda L.
    REGISTRATION NUMBER: 33,062
    REFERENCE/DOCKET NUMBER: MOBT:193
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (713) 787-1400
    TELEFAX: (713) 787-1440
  INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
```

LENGTH: 189 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-010-731-18

Alignment Scores:  
Pred. No.: 1,34e-20 Length: 189  
Score: 194.00 Matches: 31  
Percent Similarity: 87.18% Conservative: 3  
Best Local Similarity: 79.49% Mismatches: 5  
Query Match: 79.51% Indels: 0  
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-18 (1-189)

OY 2 Thrcysgluasnleualasnthrtyrarglyprocyspheglyglycysasphehis 21  
|||||  
DB 66 ACATGTGAGAAATTGGCAGATAATATAGGGGACCATGCTTTAGTGTTGTGACACTC 125  
|||||

OY 22 Cyslysthrlysgluhislleulserglyarqcyarqaspsaspphearqcy 40  
|||||

DB 126 TGCACACCAAGAGACGCGATTAGTGAAGGTGATGAGGACGACCTTCCGCTGCTGC 182  
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RESULT 4  
US-10-010-731-5  
Sequence 5, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Mu, Yonnie S.  
Rosenberger, Cindy A.  
Hakim, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,731  
FILING DATE: 13-No. US20030041347A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/003,198  
FILING DATE: 07-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT:193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 200 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 17

OTHER INFORMATION: /mod\_base= OTHER  
/note= "N" = A or C or G or T"  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-010-731-5

Alignment Scores:  
Pred. No.: 1,44e-20 Length: 200  
Score: 194.00 Matches: 31  
Percent Similarity: 87.18% Conservative: 3  
Best Local Similarity: 79.49% Mismatches: 5  
Query Match: 79.51% Indels: 0  
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-5 (1-200)

OY 2 Thrcysgluasnleualasnthrtyrarglyprocyspheglyglycysasphehis 21  
|||||  
DB 83 ACATGTGAGAAATTGGCAGATAATATAGGGGACCATGCTTTAGTGTTGTGACACTC 142  
|||||

OY 22 Cyslysthrlysgluhislleulserglyarqcyarqaspsaspphearqcy 40  
|||||

DB 143 TGCACACCAAGAGACGCGATTAGTGAAGGTGATGAGGACGACCTTCCGCTGCTGC 199  
|||||

RESULT 5  
US-09-805-694B-5  
Sequence 5, Application US/09805694B  
Publication No. US20030041350A1  
GENERAL INFORMATION:  
APPLICANT: Kinney, Anthony  
TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans  
FILE REFERENCE: B11432 US NA  
CURRENT APPLICATION NUMBER: US/09/805,694B  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/189,823  
PRIOR FILING DATE: 2000-03-16  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 5  
LENGTH: 494  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (9)  
OTHER INFORMATION: n = A, C, G, or T  
NAME/KEY: unsure  
LOCATION: (388)  
OTHER INFORMATION: n = A, C, G, or T  
NAME/KEY: unsure  
LOCATION: (392)-(393)  
OTHER INFORMATION: n = A, C, G, or T  
NAME/KEY: unsure  
LOCATION: (460)  
OTHER INFORMATION: n = A, C, G, or T  
NAME/KEY: unsure  
LOCATION: (463)  
OTHER INFORMATION: n = A, C, G, or T  
NAME/KEY: (468)  
LOCATION: (468)  
OTHER INFORMATION: n = A, C, G, or T  
OTHER INFORMATION: n = A, C, G, or T  
US-09-805-694B-5

Alignment Scores:  
Pred. No.: 1,78e-19 Length: 494  
Score: 190.00 Matches: 33  
Percent Similarity: 85.00% Conservative: 1  
Best Local Similarity: 82.50% Mismatches: 4  
Query Match: 77.87% Indels: 2  
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-09-805-694B-5 (1-494)

OY 2 Thrcysgluasnleualasnthrtyrarglyprocysphe-----glyglycysasp 19

Db 133 ACTTGCAGAACCTGGGTATACATACAGGAGTCCATGCTTCCACACTGCGAGCTGCAT 192  
QY 20 Phehscyslsthrltysgluhislsleulsercylvargcysargaspapppheargcys 39  
Db 193 GATCAGTCGCAAGAACAGACGACTTCTCTAGAGGCGATGCGAGCGATTTTCGGCTGT 252

## RESULT 6

US-10-010-731-13  
Sequence 13, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:

APPLICANT: Liang, Jihong  
Shah, Dillip Maganlal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ. ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ. ID NO: 13:

US-10-010-731-13

Alignment Scores:  
Pred. No.: 4.24e-19 Length: 250  
Score: 185.00 Matches: 30  
Percent Similarity: 86.84% Conservative: 3  
Best Local Similarity: 78.95% Mismatches: 5  
Query Match: 75.82% Indels: 0  
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-13 (1-250)

QY 2 ThhCysgluansleulaasnthrTyragGlyProCysPheGlyGlyCysaspphehis 21  
Db 108 ACATGTGAGAAATTTGGCAGATAATATAGGCGACCATGCTTAGTGCTGTGACACTCAC 167

QY 22 CysLsthrlysgluhlsleulsercylvargcysargaspapppheargcys 39  
Db 168 TGCACACCAAGAACGACGATTAGTGAAGGTGAGGACGACACTTCCGCTGC 221

RESULT 7  
US-10-010-731-19  
Sequence 19, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:

APPLICANT: Liang, Jihong  
Shah, Dillip Maganlal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ. ID NO: 19:

US-10-010-731-19

Alignment Scores:  
Pred. No.: 9.86e-19 Length: 490  
Score: 185.00 Matches: 30  
Percent Similarity: 86.84% Conservative: 3  
Best Local Similarity: 78.95% Mismatches: 5  
Query Match: 75.82% Indels: 0  
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-19 (1-490)

QY 2 ThhCysgluansleulaasnthrTyragGlyProCysPheGlyGlyCysaspphehis 21  
Db 159 ACATGTGAGAAATTTGGCAGATAATATAGGCGACCATGCTTAGTGCTGTGACACTCAC 218

QY 22 CysLsthrlysgluhlsleulsercylvargcysargaspapppheargcys 39  
Db 219 TGCACACCAAGAACGACGATTAGTGAAGGTGAGGACGACACTTCCGCTGC 272

RESULT 8  
US-10-010-731-10  
Sequence 10, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:

APPLICANT: Liang, Jihong  
Shah, Dillip Maganlal

```

: Wu, Yonnie S.
: Rosenberger, Cindy A.
: Hakimi, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: Controlling Plant Pathogenic Fungi.
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION NUMBER: US/10/010,731
: FILING DATE: 13-NO. US20030041347A1-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/003,198
: FILING DATE: 07-JAN-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT:193
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713) 787-1400
: TELEFAX: (713) 787-1440
: INFORMATION FOR SEQ. ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 507 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: one of (17, 424, 485)
: OTHER INFORMATION: /mod_base= OTHER
: /note= "N" = A or C or G or T"
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-731-10

Alignment Scores:
Pred. No.: 1.03e-18 Length: 507
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 75.82% Indels: 0
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-10 (1-507)

QY 2 ThrcysgluslnleuAlaasnTrTyArgGlyProCysPheGlyGlyCysAspPheHis 21
: |||||
DB 176 ACATGTGAGATTTGGAGATTAATATAGGGACCATGCTTGTGTGACACATCACC 235
: |||||

QY 22 CysLysThrTySGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39
: |||||
DB 236 TGCACACACAAAGACGACGATTAAGTGAAGGTGTGAGGACGACTTCGCTGC 289
: |||||

RESULT 9
US-10-178-213-436
: Sequence 436, Application US/10178213
: Publication No. US20030041348A1
: GENERAL INFORMATION:
: APPLICANT: Simmons, Carl R.
: APPLICANT: Navarro Acevedo, Pedro A.
: APPLICANT: Harvell, Leslie
: APPLICANT: Cahoon, Rebecca

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: APPLICANT: McCutchen, Billy Fred
: APPLICANT: Lu, Albert
: APPLICANT: Herrmann, Rafael
: APPLICANT: Wong, James
: TITLE OF INVENTION: Defensin Polynucleotides and Methods of
: FILE REFERENCE: 35718/246703
: CURRENT APPLICATION NUMBER: US/10/178,213
: CURRENT FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: 60/300,152
: PRIOR FILING DATE: 2001-06-22
: PRIOR APPLICATION NUMBER: 2001-06-22
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 436
: LENGTH: 420
: TYPE: DNA
: ORGANISM: Cyamopsis tetragonoloba
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (31)...(264)
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: (118)...(261)
US-10-178-213-436

Alignment Scores:
Pred. No.: 1.36e-18 Length: 420
Score: 183.50 Matches: 32
Percent Similarity: 85.37% Conservative: 3
Best Local Similarity: 78.05% Mismatches: 3
Query Match: 75.20% Indels: 3
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-10-178-213-436 (1-420)

QY 2 ThrcysgluslnleuAlaasnTrTyArgGlyProCysPheGlyGlyCys 18
: |||||
DB 121 ACATGTGAGATTTGGAGATTAATATAGGGACCATGCTTGTGTGACACGACGCTGC 180
: |||||

QY 19 AspPheHisCysLysThrTySGluHisLeuSerGlyArgCysArgAspAspPheArg 38
: |||||
DB 181 AACGATCAGTCGACAGAACAAAGACGACCTGCTCAGCGAAGGTGCAGAGAGATTTCGC 240
: |||||

QY 39 Cys 39
: |||||
DB 241 TGC 243

RESULT 10
US-10-178-213-439
: Sequence 439, Application US/10178213
: Publication No. US20030041348A1
: GENERAL INFORMATION:
: APPLICANT: Simmons, Carl R.
: APPLICANT: Navarro Acevedo, Pedro A.
: APPLICANT: Harvell, Leslie
: APPLICANT: Cahoon, Rebecca
: APPLICANT: McCutchen, Billy Fred
: APPLICANT: Lu, Albert
: APPLICANT: Herrmann, Rafael
: APPLICANT: Wong, James
: TITLE OF INVENTION: Defensin Polynucleotides and Methods of
: FILE REFERENCE: 35718/246703
: CURRENT APPLICATION NUMBER: US/10/178,213
: CURRENT FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: 60/300,152
: PRIOR FILING DATE: 2001-06-22
: PRIOR APPLICATION NUMBER: 2001-06-22
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0

```

SEQ ID NO 439  
LENGTH: 563  
TYPE: DNA  
ORGANISM: Cymamopsis tetragonoloba  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (106)...(333)  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (190)...(330)  
US-10-178-213-439

Alignment Scores:  
Pred. No.: 2,34e-18 Length: 563  
Score: 183.00 Matches: 31  
Percent Similarity: 87.50% Conservative: 4  
Best Local Similarity: 77.50% Mismatches: 3  
Query Match: 75.00% Indels: 2  
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-10-178-213-439 (1-563)

QY 2 ThTCysGluAsnLeuAlaAsnThrTyArgGlyProCysPhe-----GlyGlyCysAsp 19  
Db 193 ACATGTGAGAGTCTGGACACATACAGGGACCTGTTTACACAGATGCTGCGCAT 252  
QY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39  
Db 253 GATCAGCTGCAAGCAAGACAGCACTTAATCATGTGGAAGATGACAGAAATGATTTTCGCTGT 312

RESULT 11  
US-10-010-731-9  
Sequence 9, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shan, Diliip Meganlal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010.731  
FILING DATE: 13-No. US20030041347A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/003,198  
FILING DATE: 07-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MORT-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 327 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified base  
LOCATION: one of (244, 305)  
OTHER INFORMATION: /mod\_base= OTHER  
/note= "N" = A or C or G or T"  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-010-731-9

Alignment Scores:  
Pred. No.: 7.43e-17 Length: 327  
Score: 171.00 Matches: 28  
Percent Similarity: 86.11% Conservative: 3  
Best Local Similarity: 77.78% Mismatches: 5  
Query Match: 70.08% Indels: 0  
DB: 9 Gaps: 0

US-10-010-731-14 (1-40) x US-10-010-731-9 (1-327)

QY 4 GluAsnLeuAlaAsnThrTyArgGlyProCysPheGlyGlyCysAspPheHisCysLys 23  
Db 1 GAGATTTGGCGGAGTAAGTATAGGGACATGCTTATGTTGTGTGACACTCAGTCACCA 60  
QY 24 ThrLysGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys 39  
Db 61 ACCAAAGAGAACGACGCTTACTGGAAGCTGTAGGAGATGACTTTCGTTCT 108

RESULT 12  
US-09-759-584-35  
Sequence 35, Application US/09759584  
Patent No. US20010014732A1  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, ROBERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/759,584  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/377,687  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 141 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

```
; MOLECULE TYPE: cDNA
US-09-759-584-35

Alignment Scores:
Pred. No.: 5.76e-16 Length: 141
Score: 162.00 Matches: 27
Percent Similarity: 77.50% Conservative: 4
Best Local Similarity: 67.50% Mismatches: 7
Query Match: 66.39% Indels: 2
DB: 10 Gaps: 1

US-10-010-731-14 (1-40) x US-09-759-584-35 (1-141)

OY 2 ThrcysgluasnleuAlaasnThrTyArgGlyProCysPhe-----GlyGlyCysasp 19
|||||
Db 4 ACTTGCAGAACCTTTCTGCACTTCAAGGACCATGCTCCAGATGGAACTGCAC 63
|||||

OY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39
|||||
Db 64 AAGCATGTGCAAGAACAGACGACGACTCTTCTGGAAGATGACAGATGATTCNNNTGC 123
|||||

RESULT 13
US-10-178-213-379
; Sequence 379, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Mong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178, 213
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 379
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Cyamopsis tetragonoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(256)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (116)...(253)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379

Alignment Scores:
Pred. No.: 5.06e-12 Length: 464
Score: 140.00 Matches: 24
Percent Similarity: 80.00% Conservative: 5
Best Local Similarity: 68.57% Mismatches: 4
Query Match: 57.38% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-14 (1-40) x US-10-178-213-379 (1-464)

OY 2 ThrcysgluasnleuAlaasnThrTyArgGlyProCysPhe-----GlyGlyCysasp 19
|||||
```

```
Db 119 ACATGTGAGAGTCCGGACACACATACAGGGGACCTGTTTCACTGAGGCTAGCTGCAT 178
OY 20 PheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArg 34
|||||
Db 179 GATCATTTGCAAGAACAGACACTTATATCAGTGAACATGCACA 223
|||||

RESULT 14
US-10-178-213-100
; Sequence 100, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Mong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178, 213
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Tulipa fosteriana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)...(225)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (91)...(222)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 147, 366, 371, 392, 396, 398, 415, 432, 438, 447, 453, 455,
; LOCATION: 458
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-100

Alignment Scores:
Pred. No.: 0.00075 Length: 471
Score: 85.50 Matches: 17
Percent Similarity: 53.66% Conservative: 5
Best Local Similarity: 41.46% Mismatches: 16
Query Match: 35.04% Indels: 3
DB: 9 Gaps: 2

US-10-010-731-14 (1-40) x US-10-178-213-100 (1-471)

OY 1 AlathrcysgluasnleuAlaasnThrTyArgGlyProCysPhe-----GlyGlyCys 18.
|||||
Db 91 GCAGATTGCTACAGACCGGAGGTTCACGCGCCCTTGTAGTTCCAGCGGNTGC 150
|||||

OY 19 AspPheHisCysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspPheArg 38
|||||
Db 151 GATAGTACTGCAAGATTCAGAGACGGCTCTCAGAGAGGGTCTTGC---AGCGGCTTCAAG 207
|||||

OY 39 Cys 39
|||||
Db 208 TGC 210

RESULT 15
US-10-178-213-106
; Sequence 106, Application US/10178213
; Publication No. US20030041348A1
```

```

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Canoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178.213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 106
LENGTH: 441
TYPE: DNA
ORGANISM: Tulipa gesneriana
FEATURE:
NAME/KEY: CDS
LOCATION: (44)...(253)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (119)...(250)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 24, 270, 294, 423
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-106

```

Alignment Scores:	
Pred. No.:	0.00367
Score:	80.50
Percent Similarity:	51.22%
Best Local Similarity:	41.46%
Query Match:	32.99%
DB:	9
length:	444
Matches:	17
Conservative:	4
Mismatches:	17
Indels:	3
Gaps:	2

US-10-010-731-14 (1-40) x US-10-178-213-106 (1-441)

QY	1	AlaThrCysGluAsnLeuAlaAsnThrGlyArgGlyProCysPhe-----GlyGlyCys	18
		:::	
Db	119	GCGGATGCTGTACAGACCGAGCGGAGATTACCCAGCGCCCTGCTTGATTGCGAGGGGTGC	178
QY	19	AspPheHisCysGlyAsnThrGlyGluHisLeuLeuSerGlyArgCysAsnArgAspAspPheArg	38
		:::	
Db	179	GATAGTACTCGCAATTTACGAGACGGGAACCAAGAGGAACTTGC---AGCGGCTTCGC	235
QY	39	Cys	39
Db	236	TGC	238

Search completed: June 21, 2003, 09:04:37  
Job time : 97.8824 secs









Oy	ThcCysgluLsnleuLlaLsnthrrYrArggLYpRocgSpheGLyCysAspPheIis 21
Db	108 ACATGTCAGATTGGACGATTAATATACGGACCATGCTTAAAGTGTTGCACACTCAC 167
Oy	22 CysLysThrYrSGluLhIstLeuSerGLyArGcYsArGAspSPheArGcYs 39
Db	168 TGCACAAACCAAGACGACGAGTTAGTGAAGGTGAGGACGACTTCGCTGC 221
RESULT 5	
AAV39186	
ID	AAV39186 standard; DNA: 490 BP.
XX	AAV39186;
XX	01-OCT-1998 (first entry)
DE	Antifungal polypeptide AlfAFP1 encoding cDNA.
KW	Antifungal polypeptide: alfalfa plant; Medicago: fungal resistance;
XX	plant pathogenic fungus; AlfAFP1; AlfAFP2; ss.
OS	Medicago sativa.
XX	
XX	Key Location/Qualifiers
FT	CDS 75..293
FT	/*tag- a
FT	/transl_except- (pos:129..131, aa:Glu)
FT	/product- "AlfAFP1 polypeptide"
FT	s1g_peptide 75..135
FT	/*tag- b
FT	mat_peptide 156..290
XX	/*tag- c
PN	MO9826083-A1.
XX	
PD	18-JUN-1998.
XX	
PF	11-DEC-1997; 97MO-US2662.
XX	
PR	13-DEC-1996; 96US-0766355.
XX	
PA	(MONS ) MONSANTO CO.
XX	
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
DR	WPI: 1998-348537/30.
XX	P-PSDB: AAM61967.
PT	Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT	- used to control plant pathogenic fungi and to produce transformed
PT	plants with increased fungal resistance
PS	Claim 5; Fig 1; 97bp; English.
XX	
XX	This cDNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC	alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2 are
CC	useful to control plant fungi, especially pathogenic fungi, by
CC	transforming plant cells with a vector comprising sequences encoding
CC	AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC	of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC	cotton and especially potato. Micro-organisms may also be transformed
CC	to produce the polypeptides, and applied to plants to control plant
CC	fungi. The polypeptides, and also included with a suitable solvent in
CC	antifungal compositions and these can be administered to plants to
CC	control plant fungi. Such compositions and genetically engineered plants
CC	may also contain additional molecules e.g. the compositions can contain
CC	other antifungal agents or the plants contain DNA encoding insecticidal
CC	(e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC	to prepare antibodies useful to detect polypeptides or isolate other
CC	alfalfa plant, antifungal protein antigens. The nucleic acids are useful
CC	to produce polypeptides and transgenic plants and as probes or primers in
CC	nucleic acid hybridisation e.g. to detect complementary sequences in

CC	sample, and to prepare mutants or isolate similar sequences from related
CC	species.
XX	
SO	Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other;
	Alignment Scores:
	Pred. No.: 2,83e-16 Length: 490
	Score: 185.00 Matches: 30
	Percent Similarity: 86.84% Conservative: 3
	Best Local Similarity: 78.95% Mismatches: 5
	Query Match: 75.82% Indels: 0
	DB: 19 Gaps: 0
	US-10-010-731-14 (1-40) x AAV39186 (1-490)
OY	2 ThrcysgluaslnleuAlaasnThrryrgrGlyProCysPheGlyGlyCysAspPheHis 21
DB	159 ACATGTGAGAAATTTCGCAGATTAATATAGGGACCATGCTTTAGTGTGTTGATCATCTCAC 218
OY	22 CysLstYthrLysGlnHisLeuIeuSerGlyArgCysArgAspAspPheArgCys 39
DB	219 TGCACACCAAAAGAGACGACGATGTAGTGCAGCTGAGGAGCAGACTTCGCGTGC 272
	RESULT 6
ID	AAV39195 standard; DNA: 507 BP.
AC	AAV39195;
XX	
DT	25-SEP-1998 (first entry)
XX	
DE	Antifungal polypeptide AlfaFP1 mature sequence encoding DNA.
XX	
KW	Antifungal polypeptide; alfalfa plant; Medicago: fungal resistance;
XX	plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
OS	Medicago sativa.
XX	
XX	
FN	Key Location/Qualifiers
FT	CDS 173..310
FT	/*tag= a
FT	/product= "mature AlfaFP1"
XX	
PN	WO9826083-A1.
XX	
PD	18-JUN-1998.
XX	
PE	11-DEC-1997; 97WO-US22662.
XX	
PR	13-DEC-1996; 96US-0766355.
XX	
PA	(MONS ) MONSANTO CO.
XX	
PI	Hakimi S, Llang J, Rosenberger CA, Shah DM, Wu YS;
XX	
DR	WPI; 1998-348537/30.
DR	P-PSDB; AAW61964.
XX	
XX	
PT	Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT	- used to control plant pathogenic fungi and to produce transformed
PT	plants with increased fungal resistance
XX	
PS	Claim 5; Page 77; 97pp; English.
XX	
CC	This DNA encodes an antifungal polypeptide, AlfaFP1 isolated from
CC	alfalfa plants (Medicago). The polypeptides AlfaFP1 and AlfaFP2 are
CC	useful to control plant fungi, especially pathogenic fungi, by
CC	transforming plant cells with a vector comprising sequences encoding
CC	AlfaFP1 or AlfaFP2 to allow expression of antifungally effective amounts
CC	of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC	cotton and especially potato. Micro-organisms may also be transformed
CC	to produce the polypeptides, and applied to plants to control plant
CC	fungi. The polypeptides can also be included with a suitable solvent in

CC antifungal compositions and these can be administered to plants to  
CC control plant fungi. Such compositions and genetically engineered plants  
CC may also contain additional molecules e.g. the compositions can contain  
CC other antifungal agents or the plants contain DNA encoding insecticidal  
CC (e.g. *Bacillus thuringiensis*) proteins. The polypeptides are also useful  
CC to prepare antibodies useful to detect polypeptides or isolate other  
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
CC to produce polypeptides and transgenic plants and as probes or primers in  
CC nucleic acid hybridisation e.g. to detect complementary sequences in  
CC samples, and to prepare mutants or isolate similar sequences from related  
CC species.  
XX  
SQ Sequence 507 BP; 181 A; 85 C; 102 G; 136 T; 3 other;  
  
Alignment Scores:  
Pred. No.: 2,96e-16 Length: 507  
Score: 185.00 Matches: 30  
Percent Similarity: 86.84% Conservative: 3  
Best Local Similarity: 78.95% Mismatches: 5  
Query Match: 75.82% Indels: 0  
DB: 19 Gaps: 0  
  
US-10-010-731-14 (1-40) x AAV39195 (1-507)  
  
OY 2 ThrcysgluasnlleaualaaSnThrTyrArgGlyProCysPheGlyGlyCysAspPheHis 21  
DB 176 ACATGTGAGATTGGCAGATAAATATAGGGACCAATGCTTACGTGTGGACACATCAC 235  
||| ||||||||||| : : : ||||||||||| ||||| |||  
OY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39  
DB 236 TGCACACCAAGAGAACGCGAGTTAGTGAAGGTGTAGGCGACGACTTCCGCTGC 289  
||| ||||||||||| : : : ||||||||||| ||||||||||| ||||| |||  
  
RESULT 7  
AAZ49412  
ID AAZ49412 standard; cDNA: 468 BP.  
XX  
AC AAZ49412;  
XX  
DT 04-APR-2000 (first entry)  
XX  
DE Pea defensin protein Drr230, encoding cDNA.  
XX  
KW Transgenic plant; disease resistance: DRR206; defensin; Drr230; PR10.1;  
KW chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;  
KW CAMV 35S inducible promoter; T-DNA; bacterial/fungal pathogen;  
KW *Leptosphaeria maculans*; *Rhizoctonia solani*; *Sclerotinia sclerotiorum*; ds.  
XX  
OS *Pisum sativum*.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 78..296  
FT /\*tag= a  
FT /product= "Pea Defensin protein, Drr230"  
FT /note= "Confers resistance against fungal and bacterial  
FT pathogens"  
XX  
XX  
PD WO200001824-A2.  
XX  
PN 13-JAN-2000.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-CA00608.  
XX  
PR 03-JUL-1998; 98CA-2242116.  
PR 06-JUL-1998; 98US-0091751.  
XX  
XX  
PA (UYMA-) UNIV MANITOBA.  
XX  
PI Frisensky B, Wang Y;  
XX  
DR WPI: 2000-126938/11.  
DR P-PSDB; AAY44509.  
XX  
PT Recombinant expression system for expressing DRR206 or defensin, used

PT to produce pathogen resistant *Brassica napus* -  
XX  
XX  
PS Claim 11; Fig 9; 39pp; English.  
XX  
CC The present sequence is the cDNA encoding defensin protein, derived from  
CC the clone Drr230 of Pea. This sequence is strongly induced by bacterial  
CC and fungal pathogens like, blackleg fungus. This gene is used in a  
CC recombinant expression system, capable of transforming plants like,  
CC Canola (*Brassica napus*), under the constitutive control of CAMV 35S  
CC inducible promoter, responsive to pathogen infections. T-DNA sequence is  
CC also present, for integration of the expression system into the plant  
CC genome. Transgenic plants expressing DRR206 and defensin protein,  
CC inhibited fungal growth in-vitro and are resistant to pathogenic  
CC infections of *Rhizoctonia solani*, *Leptosphaeria maculans* and *Sclerotinia  
CC sclerotiorum*.  
XX  
SQ Sequence 468 BP; 153 A; 88 C; 84 G; 143 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 4.61e-15 Length: 468  
Score: 176.00 Matches: 28  
Percent Similarity: 86.84% Conservative: 5  
Best Local Similarity: 73.68% Mismatches: 5  
Query Match: 72.13% Indels: 0  
DB: 21 Gaps: 0  
  
US-10-010-731-14 (1-40) x AAZ49412 (1-468)  
  
OY 2 ThrcysgluasnlleaualaaSnThrTyrArgGlyProCysPheGlyGlyCysAspPheHis 21  
DB 162 ACATGTGAGATTGGCGGTTCATATPAGGAGAGTATGCTTCGGTGGATGACCGTCAC 221  
||| ||||||||||| : : : ||||||||||| ||||||||||| ||||| |||  
OY 22 CysLysThrLysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39  
DB 222 TGTAGACACCAAGAGGCGCAATTAGCGCGAGATGACGATGACTTCCGCTGT 275  
||| ||||||||||| : : : ||||||||||| ||||||||||| ||||| |||  
  
RESULT 8  
AAV39194  
ID AAV39194 standard; DNA: 327 BP.  
XX  
AC AAV39194;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Antifungal polypeptide AlfaFP2 3' region.  
XX  
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;  
KW plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.  
XX  
XX  
OS Medicago sativa.  
XX  
OS  
XX  
PN WO9826083-A1.  
XX  
PD 18-JUN-1998.  
XX  
PF 11-DEC-1997; 97WO-US22662.  
XX  
PR 13-DEC-1996; 96US-0766355.  
XX  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI Hakiml S, Liang J, Rosenberger CA, Shah DW, Wu YS;  
XX  
DR WPI: 1998-348537/30.  
XX  
XX  
PT Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)  
PT - used to control plant pathogenic fungi and to produce transformed  
PT plants with increased fungal resistance  
XX  
XX  
PS Claim 18; Page 77; 97pp; English.  
XX  
CC This sequence represents the 3' region of the DNA encoding an antifungal  
CC polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The

CC polypeptides AlfAP1 and AlfAP2 are useful to control plant fungi,  
 CC especially pathogenic fungi, by transforming plant cells with a vector  
 CC comprising sequences encoding AlfAP1 or AlfAP2 to allow expression of  
 CC antifungal effective amounts of the polypeptide. Such transformed  
 CC plants may be e.g. apple, wheat, cotton and especially potato.  
 CC Micro-organisms may also be transformed to produce the polypeptides, and  
 CC applied to plants to control plant fungi. The polypeptides can also be  
 CC included with a suitable solvent in antifungal compositions and these can  
 CC be administered to plants to control plant fungi. Such compositions and  
 CC genetically engineered plants may also contain additional molecules e.g.  
 CC the compositions can contain other antifungal agents or the plants  
 CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)  
 CC proteins. The polypeptides are also useful to prepare antibodies useful  
 CC to detect polypeptides or isolate other alfalfa plant antifungal protein  
 CC antigens. The nucleic acids are useful to produce polypeptides and  
 CC transgenic plants and as probes or primers in nucleic acid hybridisation  
 CC e.g. to detect complementary sequences in samples, and to prepare mutants  
 CC or isolate similar sequences from related species.

SQ Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other;

#### Alignment Scores:

Pred. No.:	1-42e-14	Length:	327
Score:	171.00	Matches:	28
Percent Similarity:	86.11%	Conservative:	3
Best Local Similarity:	77.78%	Mismatches:	5
Query Match:	70.08%	Indels:	0
DB:	19	Gaps:	0

US-10-010-731-14 (1-40) x AAV39194 (1-327)

OY 4 GluAsnLeuAlaAsnThrTyArgGlyProCysPheGlyGlyCysAspPheHisCysLys 23  
 DB 1 GAGATTGGGCGAATAAGTATAGGGACCATGCTTACTGTTGACACACACACGACACA 60

OY 24 ThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39  
 DB 61 ACCAAGAGAAAGCGAGTGTAGTGAAGGTGTAGGATGATCTTCGTTGT 108

#### RESULT 9

AAQ70126 ID AAQ70126 standard; cDNA: 141 BP.

AC AAQ70126;

DT 14-FEB-1995 (first entry)

DE Antimicrobial Lc-AFP.

KW Antimicrobial; Lc-AFP; symbiosis; disease-resistance;

KW fungus-resistance; *Clavibacter xyli* subsp. *cynodontis*; CXC;

KW crop improvement; endophyte; ss

OS *Lathyrus ciceria*.

PN W09416076-A.

PD 21-JUL-1994.

PF 05-JAN-1994; 94WO-GB00012.

PR 08-JAN-1993; 93GB-0000281.

PA (ZENEC) ZENECA LTD.

PI Dubock AC, Powell KA, Rees SB;

DR WPI; 1994-249223/30.

DR P-PSDB; AAR57322.

PT Antimicrobial protein producing endo-symbiotic microorganisms -  
 PT is produced by combining nucleic acids encoding the protein with  
 PT an endophyte, useful for protecting plant hosts from esp. fungal

PT disease  
 XX  
 PS Disclosure; Page 30; 39pp; English.

CC Plant-derived antimicrobial proteins are expressed in endosymbiotic  
 CC *Clavibacter xyli* subsp. *cynodontis* (CXC). Plants or seeds treated  
 CC with recombinant CXC are protected against fungal disease. A  
 CC suitable antimicrobial protein is Lc-AFP from *L. ciceria*. A  
 CC possible predicted sequence for the Lc-AFP gene is given in AAQ70126.

SQ Sequence 141 BP; 43 A; 30 C; 32 G; 33 T; 3 other;

#### Alignment Scores:

Pred. No.:	8-42e-14	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2
DB:	15	Gaps:	1

US-10-010-731-14 (1-40) x AAQ70126 (1-141)

OY 2 ThrCysGluAsnLeuAlaAsnThrTyArgGlyProCysPhe-----GlyGlyCysasp 19  
 DB 4 ACTTCGAGAACCTTCTGCAAGCTTCAAGGACCATGATCCAGATGGAACGCAAC 63

OY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39  
 DB 64 AAGCATTCGAAGAACACACAGCATCTCTTCTGGAAGATGATGATGATTCNNNTGC 123

#### RESULT 10

AAQ38648 ID AAQ38648 standard; DNA: 138 BP.

AC AAQ38648;

DT 07-JUL-1993 (first entry)

DE Encodes antifungal protein Lc-AFP1.

KW *Raphanus sativus*; Brassica; Arabidopsis; *Calceol*; *Lathyrus*; *Clitoria*;

KW fungicide; bactericide; antibiotic; antifungal; gram positive;

KW plant disease resistance; low toxicity.

OS *Lathyrus ciceria*.

PN W09305153-A.

PD 18-MAR-1993.

PF 27-AUG-1992; 92WO-GB01570.

PR 29-AUG-1991; 91GB-0018523.

PR 13-FEB-1992; 92GB-0003038.

PR 25-JUN-1992; 92GB-0013526.

PA (ICIL) IMPERIAL CHEM IND PLC.

PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;

DR WPI; 1993-100978/12.

DR Biochemical proteins isolated from seeds of plants - e.g. brassica

PT or dahlia, useful for increasing plants' resistance to fungal and

PT bacterial diseases

PS Disclosure; Fig 31A; 110pp; English.

CC This sequence appears to encode antifungal protein Lc-AFP1 from  
CC *Lathyrus ciceria* - see AAR33760. The exact source and isolation of the  
CC sequence is unclear from the specification.

Sequence 138 BP; 43 A; 30 C; 32 G; 33 T; 0 other;

**Alignment Scores:**

Pred. No.:	2, 9e-13	Length:	18
Score:	158.00	Matches:	27
Percent Similarity:	75.61%	Conservative:	4
Best Local Similarity:	65.85%	Mismatches:	8
Query Match:	64.75%	Indels:	2
DB:	14	Gaps:	1

US-10-010-731-14 (1-40) x AAQ38648 (1-138)

```
OY      2 ThyrSGlUaSnLeuAlaAsnThrTYraRgGlyProCysPhe-----GlyGLycyasp 19
         |||||
Db      4 ACTTCGAGAACTTTCGAACTTCAAGGCACATGATTCAGATCGAATACTGCAC 63
```

Qy 20 PhehiscyslysthrLysgluhisLeuSerGlyArgcysargaspaspheargcys 39  
 |||||  
 Db 64 AACGATTGGAAGAACACGACGATCTTCTTGTGGAAGATGAGAGATGATTCTGTGG 123

QY	40	CYS	40
	111		
Db	124	TGC	126

RESULT 11
AAI97313/C
ID AAI97313 standard; cDNA; 807 BP.

AC	AA197313;
XX	
DT	13-NOV-2001 (first entry)

DE	Human neuroblastoma expressed polynucleotide seq	ID NO 3388
XX		
KW	Human; neuroblastoma; malignancy; cancer; tumour marker; N-r	

OS	Homo sapiens.
XX	
PN	WO200166719-A1.

PT Nucleic acids originating in gene expressed in human neuroblastoma,  
PT useful as probe or primer in diagnosing prognosis of human  
PT neuroblastoma, malignancy and susceptibility indicator or tumour marker  
PT for anti-cancer agents -

PS Claim 1; Page 2459-2460; 2979pp; Japanese.

CC The invention relates to novel genes (A11933926-A1197963) expressed in  
CC human neuroblastoma. The nucleic acids are applicable as a probe or  
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
CC susceptibility indicators or tumour markers for anti-cancer agents. The  
CC gene information for diagnosing prognosis is related to factors similar  
CC to that for N-myc and TrkA genes.

**5Q** Sequence 807 BP; 163 A; 220 C; 214 G; 189 T; 21 other;

Alignment Scores:

Pred. No.:	2.11	length:	807
Score:	71.50	Matches:	17
Percent Similarity:	51.28%	Conservative:	3
Best Local Similarity:	43.59%	Mismatches:	14
Query Match:	29.30%	Indels:	5
DB:	22	Gaps:	2

US-10-010-731-14 (1-40) x AA197313 (1-807)

```

Qy      3  CysgluAsIeuAlaAsnIhTyrAaGlyProCysPheGly6IcyCysAspPheHisCys  22
      ||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      188  TGTGCTGTGCTCGCGCGATCGCGGGGACCTGCCGAGGGGGGCTG-----CATCG  135

```

```

Qy      23  LysThrLysGlnHisLeuLeuSeryIy-----ArgCysargaspasphearg 38
          ::::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      134  GTTCCACAGGTGCACATTTTCCACGGAAACAGAACTCGATGCACCTGCTCCGC 78

```

RESULT	12
AAD23627	
ID	AAD23627 standard; DNA; 2058 BP.

AC	AAD23627;
XX	
DT	07-MAR-2002 (first entry)

Human PKM zeta protein encoding DNA.

XX  
KW Human; memory enhancement; synaptic transmission; brain injury;  
KW spinal cord injury; protein kinase C; PKC; protein kinase M zeta;  
KW PKM zeta protein; traumatic stress disorder; pain; anticonvulsant  
KW phobia; epilepsy; drug addiction; alcohol addiction; analgesic;  
KW tranquilizer; vulnerable; antialcoholism; ds.  
DE

OS	Homo sapiens
XX	
FH	Key

PT Use of atypical form of protein kinase C e.g., protein kinase M zeta on  
PT protein kinase C Iota or Iambda, for enhancing memory or synaptic  
PT transmission, maintaining memory, or for treating brain or spinal cord  
PT injury -

PS Example 5; Fig 6; 41pp; English.

CC The invention relates to a method for enhancing memory or synaptic  
CC transmission, maintaining memory or treating brain and spinal cord  
CC injury in animal including humans. The method involves administering  
CC a therapeutically effective amount of an atypical form of protein  
CC kinase C (PKC) such as protein kinase M (PKM) zeta or PKC  $\zeta$  to/ $\lambda$  to/ $\delta$ .

CC PKM zeta inhibitor is useful for treating an animal suffering from  
CC traumatic stress disorder, phobia, acute or chronic pain and epilepsy.  
CC The method is also useful for treating drug or alcohol addiction and  
CC in antisense therapy. The present sequence is human PKM zeta protein  
CC encoding DNA.  
XX

SO Sequence 2058 BP; 493 A; 572 C; 610 G; 381 T; 2 other;

Alignment Scores:

Pred. No.: 6.92 Length: 2058  
Score: 71.50 Matches: 17  
Percent Similarity: 51.288 Conservative: 3  
Best Local Similarity: 43.598 Mismatches: 14  
Query Match: 29.30% Indels: 5  
DB: 24 Gaps: 2

US-10-010-731-14 (1-40) x AAD23627 (1-2058)

OY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyCysAspPheHisCys 22  
DB 1892 TGTGCTGCTGCTCCGCGGATCCGCGGACCTGCGCGAGGGGCTGT-----CATGGC 1945  
OY 23 LysThrLysGluHisLeuLeuSerGly-----ArgCysArgGspAspPheArg 38  
DB 1946 GTTTCAGAGTGCACATTTCACACGGAACAGACTGATGACACTGCTGCCG 2002

RESULT 13  
AAE21413  
ID AAF21413 standard; DNA: 2146 BP.

XX AAF21413:

DT 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2980.

XX Low adenosine antisense oligonucleotide: phosphorothioate; allergy;  
KM human; airway disorder; bronchoconstriction; lung inflammation;  
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KM immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;  
KM respiratory obstruction; pulmonary obstruction; impeded respiration;  
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
cancer; ss.

OS Homo sapiens.

XX MO200062736-A2.

XX 26-OCT-2000.

PD 24-MAR-2000; 2000MO-US08020.

PF 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX NYCE JW;

XX WPI; 2000-679539/66.

DR Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -

XX Disclosure: Page 1393-1394; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.

CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention.

SO Sequence 2146 BP; 506 A; 602 C; 633 G; 405 T; 0 other;

Alignment Scores:

Pred. No.: 7.3 Length: 2146  
Score: 71.50 Matches: 17  
Percent Similarity: 51.288 Conservative: 3  
Best Local Similarity: 43.598 Mismatches: 14  
Query Match: 29.30% Indels: 5  
DB: 21 Gaps: 2

US-10-010-731-14 (1-40) x AAF21413 (1-2146)

OY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyCysAspPheHisCys 22  
DB 1980 TGTGCTGCTGCTCCGCGGATCCGCGGACCTGCGCGAGGGGCTGT-----CATGGC 2033  
OY 23 LysThrLysGluHisLeuLeuSerGly-----ArgCysArgGspAspPheArg 38  
DB 2034 GTTTCAGAGTGCACATTTCACACGGAACAGACTGATGACACTGCTGCCG 2090

RESULT 14

AAAS3291  
ID AAA35291 standard; DNA: 2146 BP.

XX AAA35291:

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:165.

XX Human: adenosine receptor; low adenosine antisense oligonucleotide;  
KM phosphorothioate; impaired respiration; inflammation; allergy;  
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KM antiallergic; antiallergic; analgesic; hypotensive; cytostatic;  
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

XX MO200009525-A2.

XX 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.





Percent Similarity: 51.288  
 Best Local Similarity: 43.598  
 Query Match: 29.30%  
 DB: 24  
 Conservative: 3  
 Mismatches: 14  
 Indels: 5  
 Gaps: 2

US-10-010-731-14 (1-40) x ABR84761 (1-2146)

QY 3 CysGluAsnLeuAlaAsnThrTyrArgGlyProCysPheGlyGlyCysAspPheHisCys 22  
 1980 TGTGCTCGGTCGCGGCGGATCCGCGGGGACCTGCGCGAGGGGGCTGT-----CATGCG 2033  
 QY 23 LysThrLysGluHisLeuLeuSerGly-----ArgCysArgAspAspPheArg 38  
 Db 2034 GTTCCAGGTGCGACATTTTCCACGAGAAACGAACTCGATGCACTGACCTGCTCCGC 2090

Search completed: June 21, 2003, 06:22:39  
 Job time : 148.353 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 05:44:53 ; Search time 1594.35 seconds

(Without alignments)  
730.147 Million cell updates/sec

Title: US-10-010-731-14

Perfect score: 244

Sequence: 1 ATCCENLANTYRGPCFCGCDPCKTKKHLGRCRDPRCC 40

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-O/cgq2.1/USPTO.spool/US10010731/runat.17062003\_095705\_28161/app\_query.fasta.1.398  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45  
-DOCALLGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USBR=US10010731 @CGN.1.1.2566 @runat.17062003\_095705\_28161 -NCPU=6 -ICPU=3  
-DEV\_TIMOUT=120 -MARN\_TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pal:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mem:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	194	79.5	436	8 AB020613	AB020613 Vigna rad
2	190	77.9	494	6 AX252303	AX252303 Sequence
3	185	75.8	406	8 AF319468	AF319468 Medicago
4	184	75.4	459	8 VUSTRORD	X16877 Vigna ungu
5	176	72.1	363	8 AF139018	AF139018 Pisum ungu
6	176	72.1	468	8 PEADRR230A	L01578 Pea (p1230)
7	176	72.1	468	8 PPSI230	X52225 P.salivum p
8	162	66.4	141	6 A27063	A27063 L.cicera AF
9	162	66.4	141	6 A39547	A39547 Sequence 35
10	162	66.4	141	6 AR050147	AR050147 Sequence
11	162	66.4	141	6 AR130266	AR130266 Sequence
12	162	66.4	141	6 I23722	I23722 Sequence 35
13	131.5	53.9	456	6 PEADRR230B	L01579 Pisum sativ
14	131.5	53.9	456	6 PPSI139	X52224 P.salivum p
15	124	50.8	380	8 AB049718	AB049718 Pisum sat
16	124	32.2	200648	2 AL732464	AL732464 Mus muscu
17	78.5	29.7	2349	2 BC014270	BC014270 Homo sapi
18	72.5	29.7	130996	2 AC1120597	AC1120597 Homo sapi
19	72.5	29.7	159274	9 AC112651	AC112651 Homo sapi
20	72.5	29.7	171260	2 AC084351	AC084351 Homo sapi
21	71.5	29.3	527	8 GM012150	U12150 Glycine max
22	71.5	29.3	1739	9 AK097627	AK097627 Homo sapi
23	71.5	29.3	2146	6 AX286348	AX286348 Sequence
24	71.5	29.3	2146	6 AX333045	AX333045 Sequence
25	71.5	29.3	2216	9 HSPK2	Z15108 H.sapiens m
26	71.5	29.3	2216	9 AK055593	AK055593 Homo sapi
27	71.5	29.3	2216	9 BC008058	BC008058 Homo sapi
28	71.5	29.3	83777	9 AL158042	AL158042 Human DNA
29	71.5	29.3	178604	2 AL590822	AL590822 Homo sapi
30	71.5	29.3	213432	2 AC068198	AC068198 Homo sapi
31	70	28.7	159366	2 AC095562	AC095562 Rattus no
32	69.5	28.5	217775	10 AL592224	AL592224 Mouse DNA
33	69.5	28.3	162522	9 AC093839	AC093839 Homo sapi
34	69	28.3	227242	10 AC093925	AC093925 Genomic S
35	68	27.9	67994	2 AC114617	AC114617 Mus muscu
36	67.5	27.7	499	6 AX046767	AX046767 Sequence
37	67.5	27.7	517	6 AX046769	AX046769 Sequence
38	67.5	27.7	13692	3 CEL107	X14092 Caenorhabdi
39	67.5	27.7	40970	8 CER107	Z14092 Caenorhabdi
40	67.5	27.7	105680	8 AC006266	AC006266 Arabidops
41	67.5	27.7	131586	2 AC106180	AC106180 Rattus no
42	67.5	27.7	159677	2 AC113802	AC113802 Rattus no
43	67.5	27.7	178969	2 AC103190	AC103190 Rattus no
44	67.5	27.7	195837	8 ATCHRIV21	AL161509 Arabidops
45	67	27.5	214419	2 AC026076	AC026076 Homo sapi

RESULT 1

#### ALIGNMENTS

AB020613  
LOCUS AB020613 496 bp mRNA linear PLN 05-JAN-2002  
DEFINITION Vigna radiata mRNA for PDF1, complete cds.  
ACCESSION AB020613  
VERSION AB020613.1 GI:18146787  
KEYWORDS PDF1.  
SOURCE Vigna radiata (strain:B20F5 9-3-2-2) Immature seed cDNA to mRNA,  
clone\_lib:B20 clone:pdf-1.  
ORGANISM Vigna radiata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Rosidae; eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Vigna.  
REFERENCE  
1 Ishimoto, M. and Kaga, A.  
Muncheon defensin  
JOURNAL Published Only in Database (2002)  
REFERENCE 2 (bases 1 to 496)  
AUTHORS Ishimoto, M. and Kaga, A.  
TITLE Direct Submission  
JOURNAL Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National  
Agricultural Experiment Station, Laboratory of Plant Biotechnology;  
6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan  
(E-mail:ishimotoecgk@affrc.go.jp, Tel:+81-849-234100(ex.231),  
Fax:+81-849-247893)  
FEATURES  
source  
1. 496  
/organism="Vigna radiata"  
/strain="B20F5 9-3-2-2"  
/db\_xref="taxon:157791"  
/clone="pdf-1"  
/tissue\_type="Immature seed"  
/clone\_lib="B20"  
1. 496  
/gene="PDF1"  
46..273  
/gene="PDF1"  
/product="PDF1"  
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/protein\_id="BAB82453.1"  
/db\_xref="GI:18146788"  
/translation="MEKSLAGICFLFLVFAQEVWVOTEAKTCENLANTYRGPCFT  
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496  
/gene="PDF1"  
/note="17 a nucleotides"  
BASE COUNT 148 a 104 c 106 g 138 t  
ORIGIN  
polyA\_site  
/gene="PDF1"  
/note="17 a nucleotides"  
Alignment Scores:  
Pred. No.: 2.07e-17 Length: 496  
Score: 194.00 Matches: 34  
Percent Similarity: 85.00% Conservative: 0  
Best Local Similarity: 85.00% Mismatches: 4  
Query Match: 79.51% Indels: 2  
Gaps: 1  
US-10-010-731-14 (1-40) x AB020613 (1-496)  
QY 2 ThcCysGluAsnLeuAlaAsnThrYrArgGlyProCysPhe-----GlyGlyCysasp 19  
|||||  
Db 133 ACTTGGAAGAACTGGCGAATACTTACAGGGTCATGCTTCACCACTGGCAGCTGCAT 192  
20 PheHisCysLysThrIysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39  
|||||  
Db 193 GATCACTGCACAAGACAAGACACTTGAGAGATGGCAGGTGCAGGACGATTTCCGGTGT 252  
RESULT 2  
LOCUS AX252303 494 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 5 from Patent WO0168887.  
ACCESSION AX252303  
VERSION AX252303.1 GI:15985643

KEYWORDS  
SOURCE soybean.  
ORGANISM Glycine max.  
REFERENCE  
1 (bases 1 to 494)  
AUTHORS Jung, R. and Kinney, A.J.  
TITLE Hypoallergenic transgenic soybeans  
JOURNAL Patent: WO 0168887-A 5 20-SEP-2001;  
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED  
INTERNATIONAL, INC. (US)  
FEATURES  
source  
1. 494  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
BASE COUNT 153 a 97 c 103 g 134 t 7 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 7.26e-17 Length: 494  
Score: 190.00 Matches: 33  
Percent Similarity: 85.00% Conservative: 1  
Best Local Similarity: 82.50% Mismatches: 4  
Query Match: 77.87% Indels: 2  
Gaps: 1  
US-10-010-731-14 (1-40) x AX252303 (1-494)  
QY 2 ThcCysGluAsnLeuAlaAsnThrYrArgGlyProCysPhe-----GlyGlyCysasp 19  
|||||  
Db 133 ACTTGGAAGAACTGGCGAATACTTACAGGGTCATGCTTCACCACTGGCAGCTGCAT 192  
QY 20 PheHisCysLysThrIysGluHisLeuLeuSerGlyArgCysArgAspPheArgCys 39  
|||||  
Db 193 GATCACTGCACAAGACAAGACACTTGAGAGATGGCAGGACGATTTCCGGTGT 252  
RESULT 3  
LOCUS AF319468 406 bp mRNA linear PLN 14-DEC-2000  
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.  
ACCESSION AF319468  
VERSION AF319468.1 GI:11762085  
KEYWORDS  
SOURCE Medicago sativa.  
ORGANISM Medicago sativa.  
REFERENCE  
1 (bases 1 to 406)  
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., Rosenberger, C.A. and Hakimi, S.  
TITLE Antifungal Polypeptide(s) and Methods for Controlling Plant  
JOURNAL Pathogenic Fungi  
Patent: US 6121436 19-SEP-2000;  
Monsanto Company; St Louis, MO  
2 (bases 1 to 406)  
AUTHORS Gao, A.G., Hakimi, S.M., Miltanck, C.A., Wu, Y., Woerner, B.M.,  
Starr, D.M., Shah, D.M., Liang, J. and Rommens, C.M.  
TITLE Fungal pathogen protection in potato by expression of a plant  
JOURNAL Nat. Biotechnol. 18 (12), 1307-1310 (2000).  
DEFINITION defensin peptide  
ACCESSION Nat. Biotechnol. 18 (12), 1307-1310 (2000).  
VERSION 11101813  
PUBMED 20553844  
REFERENCE  
3 (bases 1 to 406)  
AUTHORS Miltanck, C.A., Wu, Y., Hakimi, S.M., Liang, J., Shah, D.M. and Gao, A.G.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway,  
St Louis, MO 63199, USA  
FEATURES  
source  
1. 406  
/organism="Medicago sativa"

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CDS
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  /note="alfAFP; defensin"
  /codon_start=1
  /product="antifungal protein precursor"
  /protein_id="AAG40321.1"
  /db_xref="GI:11762086"
  /translation="MEKSLAGLCFLFLVFAOEIVTVEARTCEMLADKRGPCFSG
  CDHCTTKENAVSGRCRDPRCWCCTKRC"
  sig_peptide
  mat_peptide
  156..290
  /product="antifungal protein"
  BASE COUNT      140 a      74 c      78 g      114 t
  ORIGIN

Alignment Scores:
Pred. No.:      2,85e-16      Length:      406
Score:          185.00      Matches:      30
Percent Similarity: 86.84%      Conservative: 3
Best Local Similarity: 78.95%      Mismatches: 5
Query Match:    75.82%      Indels:      0
DB:             8      Gaps:      0

US-10-010-731-14 (1-40) x AF319468 (1-406)

QY
  2 ThrcysgluasnlleualaasnThrYrArgGlyProCysPheGlyGlyCysaspPheHis 21
  |||||
  159 ACATGCGAGAAATTGGCAGATAATATAGGCGCCATCTGTTAGTGTGTGACACTGCAC 218
  |||||

QY
  22 CysLysThrLysgluHisLeuSerGlyArgCysArgAspAspPheArgCys 39
  |||||
  219 TCACACCAACGAAGACGACTGAGAGAGTGAGGAGACACTCCGCTGC 272
  |||||

RESULT 4
VSTORED
LOCUS      VSTORED      459 bp      mRNA      linear      PLN 12-SEP-1993
DEFINITION Vigna unguiculata cDNA for stored cotyledon mRNA.
ACCESSION X16877
VERSION    X16877.1 GI:22075
KEYWORDS
SOURCE
  Vigna radiata.
  Vigna radiata
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
  Vigna
  1 (bases 1 to 459)
  Yamauchi,D.
  Direct Submission
  Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo
  Metropolitan University, Fukazawa 2-1, Setagaya-ku, Tokyo 158,
  Japan
  2 (bases 1 to 459)
  Ishibashi,N., Yamauchi,D. and Minamikawa,T.
  Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide
  sequence of cloned cDNA for a stored mRNA and induction of its
  synthesis by precocious germination
  Plant Mol. Biol. 15 (1), 59-64 (1990)
  91355865
  2103443

FEATURES
  source
    1..459
    /organism="Vigna radiata"
    /db_xref="taxon:157791"
    /clone="PSAS10"
    /tissue_type="cotyledon"
    /clone_lib="lambda gt10"
    /dev_stage="seed"
    14..241
    /note="PSAS10 ORF"
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    /protein_id="CAA34760.1"
    /db_xref="GI:22076"
  CDS
    /db_xref="taxon:3879"
    /note="alfAFP; defensin"
    /codon_start=1
    /product="antifungal protein precursor"
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    /db_xref="GI:11762086"
    /translation="MEKSLAGLCFLFLVFAOEIVTVEARTCEMLADKRGPCFSG
    CDHCTTKENAVSGRCRDPRCWCCTKRC"
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    mat_peptide
    156..290
    /product="antifungal protein"
    BASE COUNT      140 a      74 c      78 g      114 t
    ORIGIN

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  /translation="MEKSLAGLCFLFLVFAOEIVVQSEAKTCENLVDTYRGPCFT
  TSSCDHCKNKEHLISGRCDPRCWCCTKRC"
  BASE COUNT      136 a      91 c      99 g      133 t
  ORIGIN

Alignment Scores:
Pred. No.:      4.43e-16      Length:      459
Score:          184.00      Matches:      32
Percent Similarity: 82.50%      Conservative: 1
Best Local Similarity: 80.00%      Mismatches: 5
Query Match:    75.41%      Indels:      2
DB:             8      Gaps:      1

US-10-010-731-14 (1-40) x VSTORED (1-459)

QY
  2 ThrcysgluasnlleualaasnThrYrArgGlyProCysPhe-----GlyGlyCysasp 19
  |||||
  101 ACTTGGAGAACCTGGTGATACATACAGGGGTCGCTTACACCACTGGAGCTGCAT 160
  |||||

QY
  20 PheHisCysLysThrLysgluHisLeuSerGlyArgCysArgAspAspPheArgCys 39
  |||||
  161 GATCACTGCAAGAACAAACACTTGTGATGCGAGGTGAGGATGATGTCGCGTGT 220
  |||||

RESULT 5
AF139018
LOCUS      AF139018      363 bp      mRNA      linear      PLN 02-JAN-2001
DEFINITION Pism sativum disease resistance response protein 230 precursor
(DRR230) mRNA, complete cds.
ACCESSION AF139018
VERSION    AF139018.1 GI:12002298
KEYWORDS
SOURCE
  Pism sativum.
  Pism sativum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
  Pism.
  1 (bases 1 to 363)
  Savenstrand,H., Brosche,M. and Strid,A.
  Stress-induced disease resistance response protein 230 cDNA from
  Pism sativum cv. Greenfeast
  Unpublished
  2 (bases 1 to 363)
  Savenstrand,H., Brosche,M. and Strid,A.
  Direct Submission
  Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg
  University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530,
  Sweden

FEATURES
  source
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    /cultivar="Greenfeast"
    /db_xref="taxon:3888"
    1..363
    /gene="DRR230"
    56..274
    /gene="DRR230"
    /note="ozone-induced; similar to the Pism sativum cv.
    Alaska product encoded by Genbank Accession Number I01578"
    /codon_start=1
    /product="disease resistance response protein 230
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    /protein_id="AAG43285.1"
    /db_xref="GI:12002299"
    /translation="MEKSLAGLCFLFLVFAOEIVVSEANTCENLVAGYKGVCFSG
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  ORIGIN

Alignment Scores:
Pred. No.:      4.29e-15      Length:      363
Score:          176.00      Matches:      28

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Percent Similarity: 86.84%  
Best Local Similarity: 73.68%  
Query Match: 72.13%  
DB: 8  
Conservative: 5  
Matches: 5  
Indels: 0  
Gaps: 0

US-10-010-731-14 (1-40) x AF139018 (1-363)

QY 2 ThcYsgluAsnleuAlaasnThrTYrArgGlyProCysPheGlyCysAspPheHis 21  
|||||  
DB 140 ACATGTGAGAAATTGGCTGTCATATTAAGGAGATGCTTCGGTGGATGTGACCGTCAC 159  
|||||

QY 22 CysLstThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39  
|||||  
DB 200 TGTAGAACAACAGAGCGCCGCAATTAGCGGATGAGGATGACTTTCGCTGT 253  
|||||

RESULT 6  
PEADRR230A 468 bp mRNA linear PLN 11-FEB-2002  
LOCUS  
DEFINITION  
Psa (p1230) disease resistance response protein 230 (DRR230-a)  
ACCESSION  
L01578.1 GI:169073  
VERSION  
L01578.1 GI:169073  
KEYWORDS  
cysteine-rich protein; disease resistance response protein 230;  
pathogenesis-related protein.  
SOURCE  
Pisum sativum  
ORGANISM  
Pisum sativum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;  
Pisum.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
FEATURES  
source

1 (bases 1 to 468)  
Chiang,C.C. and Hadwiger,L.A.  
The fusarium solani-induced expression of a pea gene family  
encoding high cysteine content proteins  
Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)  
92190628  
1799696  
On Feb 8, 2002 this sequence version replaced gi:247416.  
Location/Qualifiers  
1. 468  
/organism="Pisum sativum"  
/strain="Alaska"  
/db\_xref="taxon:3888"  
/tissue\_type="pod tissue treated with Fusarium solani  
conidia"  
/dev\_stage="immature"  
1. 468  
/gene="DRR230-a"  
78..296  
/gene="DRR230-a"  
/function="unknown"  
/standard\_name="pathogenesis related protein"  
/note="p1230"  
/codon\_start=1  
/evidence="experimental"  
/product="disease resistance response protein"  
/protein\_id="AA09117.1"  
/db\_xref="GI:169074"  
/translation="MEKSLACLSPFLLVFAQELVSEANTNCENLASIKYGVCRGS  
CDRHCTOGSALISGRCDPRFCMCTKNC"  
159..293  
mat\_peptide  
/gene="DRR230-a"  
/product="disease resistance response protein"  
/function="unknown"  
/note="determined by in vitro cleavage with microsomal  
membranes"  
/evidence="experimental"  
BASE COUNT 153 a 88 c 84 g 143 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5,6e-15 Length: 468  
Score: 176.00 Matches: 28

Percent Similarity: 86.84%  
Best Local Similarity: 73.68%  
Query Match: 72.13%  
DB: 8  
Conservative: 5  
Matches: 5  
Indels: 0  
Gaps: 0

US-10-010-731-14 (1-40) x PEADRR230A (1-468)

QY 2 ThcYsgluAsnleuAlaasnThrTYrArgGlyProCysPheGlyCysAspPheHis 21  
|||||  
DB 162 ACATGTGAGAAATTGGCTGTCATATTAAGGAGATGCTTCGGTGGATGTGACCGTCAC 221  
|||||

QY 22 CysLstThrLysGluHisLeuSerGlyArgCysArgAspAspPheArgCys 39  
|||||  
DB 222 TGTAGAACAACAGAGCGCCGCAATTAGCGGATGAGGATGACTTTCGCTGT 275  
|||||

RESULT 7  
PSP1230 468 bp mRNA linear PLN 09-AUG-2002  
LOCUS  
DEFINITION  
P.sativum p1230 mRNA.  
ACCESSION  
X52225  
VERSION  
X52225.1 GI:22208748  
KEYWORDS  
secreted protein.  
SOURCE  
pea.  
ORGANISM  
Pisum sativum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;  
Pisum.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
FEATURES  
source

1 (bases 1 to 468)  
Chiang,C.C. and Hadwiger,L.A.  
The fusarium solani-induced expression of a pea gene family  
encoding high cysteine content proteins  
Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)  
92190628  
1799696  
Direct Submission  
Submitted (03-AUG-1990) Chiang C., Washington State University,  
Dept. of Plant Pathology, Pullman, WA 99164-6430, USA  
Location/Qualifiers  
1. 468  
/organism="Pisum sativum"  
/db\_xref="taxon:3888"  
/tissue\_type="endocarp"  
1. 468  
/gene="p1230"  
78..296  
/gene="p1230"  
/codon\_start=1  
/product="p1230"  
/protein\_id="CAA36474.1"  
/db\_xref="GI:22208749"  
/translation="MEKSLACLSPFLLVFAQELVSEANTNCENLASIKYGVCRGS  
CDRHCTOGSALISGRCDPRFCMCTKNC"  
78..158  
sig\_peptide  
/gene="p1230"  
159..293  
mat\_peptide  
/gene="p1230"  
/product="unnamed"  
BASE COUNT 153 a 88 c 84 g 143 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5,6e-15 Length: 468  
Score: 176.00 Matches: 28  
Percent Similarity: 86.84%  
Best Local Similarity: 73.68%  
Query Match: 72.13%  
DB: 8  
Conservative: 5  
Matches: 5  
Indels: 0  
Gaps: 0  
US-10-010-731-14 (1-40) x PSP1230 (1-468)  
QY 2 ThcYsgluAsnleuAlaasnThrTYrArgGlyProCysPheGlyCysAspPheHis 21  
|||||

Db	162	ACATGTGAGAAATTGGCGTTCATATTAAGGAGATGCTTCGGTGGATGTGACCGTCC	221
Oy	22	CysLysThrIlySGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys	39
Db	222	TGTAGAACACAAAGAGGGCGCAATTAAGCGGAGATGCAGAGATGACTTCGCTGT	275
RESULT 8			
A27063			
LOCUS	A27063	AFP sequence.	141 bp
DEFINITION	A27063		linear
ACCESSION	A27063		PAT 12-JUN-1995
VERSION	A27063.1	GI:1247357	
KEYWORDS			
SOURCE			
ORGANISM			
Lathyrus cicera.			
Lathyrus cicera			
Euarystolia, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;			
Lathyrus.			
FEATURES			
source	1..141	Location/Qualifiers	
	/organism="Lathyrus cicera"		
	/db_xref="taxon:3856"		
BASE COUNT	43 a 30 c 32 g 33 t	3 others	
ORIGIN			
Alignment Scores:			
Pred. No.:	1..31e-13	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2
DB:	6	Gaps:	1
US-10-010-731-14 (1-40) x A27063 (1-141)			
Oy	2	ThrcysgluAsnLeuAlaAsnThrTyArgGlyProCysPhe-----GlyGlyCysAsp	19
Db	4	ACTTGGCGAACCCTTCTCGGAACCTTCAAGGACCATGCAATCCAGATGGAACGCAAC	63
Oy	20	PheHisCysLysThrIlySGluHisLeuLeuSerGlyArgCysArgAspAspPheArgCys	39
Db	64	AAGCATTCGCAAGAACACACAGACATCTCTTCTGTGGAGATGCAGATGATTCNNNTGC	123
RESULT 9			
A39547			
LOCUS	A39547	Sequence 35 from Patent W09416076.	141 bp
DEFINITION	A39547		DNA
ACCESSION	A39547		linear
VERSION	A39547.1	GI:2295840	PAT 05-MAR-1997
KEYWORDS			
SOURCE			
ORGANISM			
unidentified.			
unclassified.			
1 (bases 1 to 141)			
Dubock,A.C., Powell,K.A. and Rees,S.B.			
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS			
Patent: WO 9416076-A 35 21-JUL-1994;			
ZENECA LTD (GB)			
Other publication AU 5820494 940815.			
COMMENT			
FEATURES			
source	1..141	Location/Qualifiers	
	/organism="unidentified"		
	/db_xref="taxon:32644"		
BASE COUNT	43 a 30 c 32 g 33 t	3 others	
ORIGIN			
Alignment Scores:			
Pred. No.:	1..31e-13	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	7
Query Match:	66.39%	Indels:	2

DB:	6	Gaps:	1
US-10-010-731-14 (1-40) x A39547 (1-141)			
Oy	2	ThrcysgluAsnleuAlaAsnThrTyArgGlyProCysPhe-----GlyGlyCysasp	19
Db	4	ACTTGCAGAACCTTTCTGGAACCTTTCAAGGACCATTCACATGCAGATGGAACTGGCAAC	63
Oy	20	PheHisCysLysThrLysGlnHisleuSerGlyArgCysArgAspPheArgCys	39
Db	64	AAGCATTTGCAGAACGACGACCATCTTTCTGGAAGATGCAGAGATGATTCNNNTGC	123
RESULT 10			
LOCUS	AR050147	141 bp	linear
DEFINITION	Sequence 35 from patent US 5824869.		PAT 29-SEP-1999
ACCESSION	AR050147		
VERSION	AR050147.1		GI:5972139
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 141).		
AUTHORS	Broekert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B., Terras,F.R.G. and Vanderleyden,J.		
TITLE	Biocidal proteins		
JOURNAL	Patent: US 5824869-A 35 20-OCT-1998;		
FEATURES	Location/Qualifiers		
source	1..141		
BASE COUNT	43 a 30 c 32 g 33 t		3 others
ORIGIN	/organism="unknown"		
Alignment Scores:			
Pred. No.:	1,31e-13	Length:	141
Score:	162.00	Matches:	27
Percent Similarity:	77.50%	Conservative:	4
Best Local Similarity:	67.50%	Mismatches:	2
Query Match:	66.39%	Indels:	2
DB:	6	Gaps:	1
US-10-010-731-14 (1-40) x AR050147 (1-141)			
Oy	2	ThrcysgluAsnleuAlaAsnThrTyArgGlyProCysPhe-----GlyGlyCysasp	19
Db	4	ACTTGCAGAACCTTTCTGGAACCTTTCAAGGACCATTCACATGCAGATGGAACTGGCAAC	63
Oy	20	PheHisCysLysThrLysGlnHisleuSerGlyArgCysArgAspPheArgCys	39
Db	64	AAGCATTTGCAGAACGACGACCATCTTTCTGGAAGATGCAGAGATGATTCNNNTGC	123
RESULT 11			
LOCUS	AR130266	141 bp	DNA
DEFINITION	Sequence 35 from patent US 6187904.		linear
ACCESSION	AR130266		PAT 16-MAY-2001
VERSION	AR130266.1		GI:14118163
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 141)		
AUTHORS	Broekert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B., Terras,F.R.G. and Vanderleyden,J.		
TITLE	Biocidal proteins		
JOURNAL	Patent: US 6187904-A 35 13-FEB-2001;		
FEATURES	Location/Qualifiers		
source	1..141		
BASE COUNT	43 a 30 c 32 g 33 t		3 others
ORIGIN	/organism="unknown"		
Alignment Scores:			

Pred. No.: 1,31e-13 Length: 141  
Score: 162.00 Matches: 27  
Percent Similarity: 77.50% Conservative: 4  
Best Local Similarity: 67.50% Mismatches: 7  
Query Match: 66.39% Indels: 2  
DB: 6 Gaps: 1

US-10-010-731-14 (1-40) x AR130266 (1-141)

OY 2 ThrCysGluAsnLeuAlaAsnThrTYrArgGlyProCysPhe-----GlyGlyCysAsp 19  
|||||  
DB 4 ACTTGGAGAGAACCTTTCTGAGACTTTCAGAGGACCATGCTCCAGATGGAAACTGCAC 63

OY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39  
|||||  
DB 64 AACGATTGCAAGAACAGACGATCTTCTTTCGGAAGATGACAGATGATTCNNNTGC 123

RESULT 12  
LOCUS 123722 141 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 35 from patent US 5538525.  
ACCESSION 123722  
VERSION 123722.1 GI:1603592  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 141)  
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,  
Terras, F.R.G. and Vanderleyden, J.  
Biochemical proteins  
Patent: US 5538525-A 35 23-JUL-1996;  
Location/Qualifiers  
1. 141  
source /organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others  
ORIGIN

## Alignment Scores:

Pred. No.: 1,31e-13 Length: 141  
Score: 162.00 Matches: 27  
Percent Similarity: 77.50% Conservative: 4  
Best Local Similarity: 67.50% Mismatches: 7  
Query Match: 66.39% Indels: 2  
DB: 6 Gaps: 1

US-10-010-731-14 (1-40) x I23722 (1-141)

OY 2 ThrCysGluAsnLeuAlaAsnThrTYrArgGlyProCysPhe-----GlyGlyCysAsp 19  
|||||  
DB 4 ACTTGGAGAGAACCTTTCTGAGACTTTCAGAGGACCATGCTCCAGATGGAAACTGCAC 63

OY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39  
|||||  
DB 64 AACGATTGCAAGAACAGACGATCTTCTTTCGGAAGATGACAGATGATTCNNNTGC 123

RESULT 13  
PEADRR230B 456 bp mRNA linear PLN 11-FEB-2002  
LOCUS  
DEFINITION Plasm salivum disease resistance response protein 39 (DRR230-B)  
ACCESSION L01579.1 GI:169075  
VERSION L01579.1 GI:169075  
KEYWORDS cysteine-rich protein; disease resistance response protein 39;  
pathogenesis-related protein.  
SOURCE Plasm salivum (strain Alaska) CDNA to mRNA.  
ORGANISM Plasm salivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;  
Plum.  
REFERENCE 1 (bases 1 to 456)  
AUTHORS Chiang, C.C. and Hadwiger, L.A.

TITLE The Fusarium solani-induced expression of a pea gene family  
encoding high cysteine content proteins  
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)  
MEDLINE 92190628  
PUBMED 1799696  
COMMENT On Feb 8, 2002 this sequence version replaced gi:247414.  
FEATURES  
source  
1. 456  
Location/Qualifiers  
/organism="Plasm salivum"  
/strain="Alaska"  
/db\_xref="taxon:3888"  
/tissue\_type="pod tissue treated with Fusarium solani  
conidia."  
/dev\_stage="Immature"  
1. 456  
/gene="DRR230-b"  
69. 293  
/gene="DRR230-b"  
/function="unknown"  
/standard\_name="pathogenesis related protein"  
/evidence="experimental"  
/product="disease resistance response protein 39"  
/protein\_id="AA079118.1"  
/db\_xref="GI:169076"  
/translation="MEKSLALASFLLLVLEVAQRIIVTEANTCEHLADTYRGVCF  
NASCDHCKNKHALISGTCHDMKCFCTQNC"  
153. 290  
/gene="DRR230-b"  
/product="disease resistance response protein"  
/function="unknown"  
/standard\_name="pathogenesis related protein"  
/note="cysteine content determined by homology with pl230;  
putative"

mat\_peptide

BASE COUNT 155 a 81 c 79 g 141 t  
ORIGIN

## Alignment Scores:

Pred. No.: 6,5e-09 Length: 456  
Score: 131.50 Matches: 24  
Percent Similarity: 72.50% Conservative: 5  
Best Local Similarity: 60.00% Mismatches: 8  
Query Match: 53.89% Indels: 2  
DB: 8 Gaps: 3

US-10-010-731-14 (1-40) x PEADRR230B (1-456)

OY 2 ThrCysGluAsnLeuAlaAsnThrTYrArgGlyProCysPhe-----GlyGlyCysAsp 19  
|||||  
DB 156 ACTTGGAGACATTTGGCTGATACATACAGGCGATGCTTCACGAATGCTAGCTGAT 215

OY 20 PheHisCysLysThrLysGluHisLeuSerGlyArgCysArgAspPheArgCys 39  
|||||  
DB 216 GATCACTGCAAGAACAGACGACTTAATCAGTGGACGTCGCAT--GACTGGAATGT 272

RESULT 14  
PSP139 456 bp mRNA linear PLN 09-AUG-2002  
LOCUS  
DEFINITION P. sativum PL139 mRNA.  
ACCESSION X52224  
VERSION X52224.1 GI:22208744  
KEYWORDS secreted protein.  
SOURCE pea.  
ORGANISM Plasm salivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;  
Plum.  
REFERENCE 1  
AUTHORS Chiang, C.C. and Hadwiger, L.A.  
TITLE The Fusarium solani-induced expression of a pea gene family  
encoding high cysteine content proteins  
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)





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OM protein - nucleic search, using frame\_p1us\_p2n model

Run on: June 21, 2003, 05:44:53 ; Search time 1793.65 Seconds  
(without alignments)  
730.147 Million cell updates/sec

Title: US-10-010-731-2

Perfect score: 275  
Sequence: 1 RRCENMADKRYRGPCFSGCDT.....ENAVSGRCRDPFCMCTKRC 45

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame-p2n.model -DEV=x1h  
-Q=/cgn2.1/USPTO.spool/US10010731/runat.17062003\_095705\_28161/app.query.fasta\_1.398  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MTMARCH=0.1 -LOOPEXT=0  
-UNITS=bits -STRT=1 -END=1 -MATRIX=blomsun62 -TRANS=human4.cdi -LIST=45  
-DOCAALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10010731.ecgn.1.1.2566 -runat.17062003.095705.28161 -NCPU=6 -ICPU=3  
-NM\_MAP -LARGEBOOK -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONCLIG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
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2: gb\_ba:\*  
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10: gb\_pr:\*  
11: gb\_ro:\*  
12: gb\_sts:\*  
13: gb\_sy:\*  
14: gb\_un:\*  
15: gb\_vl:\*  
16: em\_ba:\*  
17: em\_fun:\*  
18: em\_hum:\*  
19: em\_in:\*  
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22: em\_ov:\*  
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24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vl:\*  
30: em\_hgt\_hum:\*  
31: em\_hgt\_inv:\*  
32: em\_hgt\_other:\*  
33: em\_hgt\_mus:\*  
34: em\_hgt\_pin:\*  
35: em\_hgt\_rod:\*  
36: em\_hgt\_mam:\*  
37: em\_hgt\_vrt:\*  
38: em\_sy:\*  
39: em\_hgt\_hum:\*  
40: em\_hgt\_mus:\*  
41: em\_hgt\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	275	100.0	406	8	AF319468
2	214	77.8	363	8	AF139018
3	214	77.8	468	8	PEADRR230A
4	214	77.8	468	8	PSPT230
5	206	74.9	494	6	AX252303
6	199	72.4	496	8	AB020613
7	197	71.6	459	8	VUSTORED
8	168	61.1	141	6	A27063
9	168	61.1	141	6	A39547
10	168	61.1	141	6	AR050147
11	168	61.1	141	6	ARI30266
12	168	61.1	141	6	I23722
13	141.5	51.5	456	8	PEADRR230B
14	141.5	51.5	456	8	PSPT39
15	141	51.3	380	8	AB049718
16	103	37.5	527	8	GMU12150
17	99	36.0	733	8	AF417297
18	95	34.5	612	8	AB034956
19	94	34.2	382	8	AB052687
20	93	33.8	439	8	AF141131
21	93	33.8	472	8	AF178634
22	92	33.5	469	8	LES133601
23	92	33.5	5461	8	CACHTIOGN
24	91	33.1	265	8	AY079405
25	91	33.1	486	8	NTDEFENS1
26	91	33.1	515	8	AY050979
27	91	33.1	93212	8	AC005936
28	90	32.7	470	8	ST332R
29	90	32.7	1561	8	PETSTHONT
30	88	32.0	526	8	AY087062
31	87	31.6	469	8	ATP11A
32	87	31.6	507	8	AF370355
33	86	31.3	481	8	BRRIIP25
34	85	30.9	403	8	OSU72942
35	85	30.9	1459	8	AF044059
36	85	30.9	154128	8	AP000615
37	83	29.8	185836	2	AP004836
38	82	29.8	512	8	AF442388
39	82	29.8	2000	6	AX461158
40	81	29.5	490	8	PASRTIGEN
41	81	29.5	1370	4	AY039681
42	80.5	29.3	85355	2	AC019557
43	80.5	29.3	172284	3	AC010018
44	80.5	29.3	178019	3	AC091206
45	80.5	29.3	180859	2	AC091126

RESULT 1

## ALIGNMENTS

AF139468  
LOCUS AF139468 406 bp mRNA linear PLN 14-DEC-2000  
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.  
ACCESSION AF139468  
VERSION AF139468.1 GI:11762085  
KEYWORDS  
SOURCE Medicago sativa.  
ORGANISM Medicago sativa.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
REFERENCE 1 (bases 1 to 406)  
AUTHORS Liang,J., Shah,D.M., Wu,Y.S., Rosenberger,C.A. and Hakiml,S.  
TITLE Antifungal Polypeptide(s) and Methods for Controlling Plant Pathogenic Fungi  
JOURNAL Patent: US 6121436 19-SEP-2000;  
Monsanto Company; St Louis, MO  
REFERENCE 2 (bases 1 to 406)  
AUTHORS Gao,A.G., Hakiml,S.M., Miltanck,C.A., Wu,Y., Woerner,B.M., Stark,D.M., Shah,D.M., Liang,J. and Rommens,C.M.  
TITLE Fungal pathogen protection in potato by expression of a plant defensin peptide  
JOURNAL Nat. Biotechnol. 18 (12), 1307-1310 (2000)  
MEDLINE 2053844  
PUBMED 11101813  
REFERENCE 3 (bases 1 to 406)  
AUTHORS Miltanck,C.A., Wu,Y., Hakiml,S.M., Liang,J., Shah,D.M. and Gao,A.G.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway, St Louis, MO 63196, USA  
FEATURES  
source 1. 406  
/organism="Medicago sativa"  
/db\_xref="taxon:3879"  
75..293  
/note="alfafp; defensin"  
/codon\_start=1  
/product="antifungal protein precursor"  
/protein\_id="AAC40321.1"  
/db\_xref="GI:11762086"  
/translation="MERKSLAGCEFLVLFVAQELIVTEARTCEMLADKYKSGPCRS  
CDHCTTKENAVSGRCRDPFCWCTKRC"  
sig\_peptide  
mat\_peptide  
BASE COUNT 140 a 74 c 78 g 114 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 3,21e-23 Length: 406  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-10-010-731-2 (1-45) x AF139468 (1-406)  
QY 1 ArgThCysGluAsnLeuAlaAspLysTYrArgGLyProCysPheSerGLyCysAspThr 20  
DB 156 AGAACATGTGAGATTGGCAGATTAATAATAGGGGACCATGCTTTAGTGGTGTGACACT 215  
QY 21 HlscYstThrThLysGluAsnAlaValSerGLyArGcYsArGAspAspPheArGcYsTTP 40  
DB 216 CACTGCACAACCAAGAGAACCCAGTAACTAGTGAGAGGTGTAAGGACACTTCGCTCTGG 275  
QY 41 CystHlyAsrGcYs 45  
DB 276 TGTACTAAAGATGT 290  
RESULT 2  
AF139018

LOCUS AF139018 363 bp mRNA linear PLN 02-JAN-2001  
DEFINITION Pisum sativum disease resistance response protein 230 precursor (DRR230) mRNA, complete cds.  
ACCESSION AF139018  
VERSION AF139018.1 GI:12002298  
KEYWORDS  
SOURCE Pisum sativum.  
ORGANISM Pisum sativum.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
REFERENCE 1 (bases 1 to 363)  
AUTHORS Sevenstrand,H., Brosche,M. and Strid,A.  
TITLE Stress-induced disease resistance response protein 230 cDNA from Pisum sativum cv. Greenfeast  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 363)  
AUTHORS Sevenstrand,H., Brosche,M. and Strid,A.  
TITLE Direct Submission  
JOURNAL Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530, Sweden  
FEATURES  
source 1. 363  
/organism="Pisum sativum"  
/cultivar="Greenfeast"  
/db\_xref="taxon:3888"  
1..363  
/gene="DRR230"  
56..274  
/gene="DRR230"  
/note="ozone-induced; similar to the Pisum sativum cv. Alaska product encoded by GenBank Accession Number L01578"  
/codon\_start=1  
/product="disease resistance response protein 230 precursor"  
/protein\_id="AAC43285.1"  
/db\_xref="GI:12002299"  
/translation="MERKSLAGCEFLVLFVAQELIVTEARTCEMLADKYKSGPCRS  
CDHCTTKENAVSGRCRDPFCWCTKRC"  
BASE COUNT 113 a 68 c 74 g 108 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 3,38e-16 Length: 363  
Score: 214.00 Matches: 33  
Percent Similarity: 81.82% Conservative: 3  
Best Local Similarity: 75.00% Mismatches: 8  
Query Match: 77.82% Indels: 0  
Gaps: 0  
US-10-010-731-2 (1-45) x AF139018 (1-363)  
QY 2 ThCysGluAsnLeuAlaAspLysTYrArgGLyProCysPheSerGLyCysAspThrHis 21  
DB 140 ACATGTGAGATTGGCTGTCATATAAGGAGATGCTGGTGGATGTGACCGTAC 199  
QY 22 CystThrThLysGluAsnAlaValSerGLyArGcYsArGAspAspPheArGcYsTTP 41  
DB 200 TGTAGAACAACAMAGAGCGCAATTAACCGCAGATGCAGGAGATGACTTTCGCTGTGTC 259  
QY 42 ThrLysArGcYs 45  
DB 260 ACTAAAACTGT 271  
RESULT 3  
PEADRR230A  
LOCUS PEADRR230A 468 bp mRNA linear PLN 11-FEB-2002  
DEFINITION pea (p1230) disease resistance response protein 230 (DRR230-a) mRNA, complete cds.  
ACCESSION L01578 588685  
VERSION L01578.1 GI:169073

KEYWORDS cysteine-rich protein; disease resistance response protein 230; pathogenesis-related protein.

SOURCE Pisum sativum.

ORGANISM Pisum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

REFERENCE 1 (bases 1 to 468)

AUTHORS Chiang, C.C. and Hadwiger, L.A.

TITLE The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins

JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)

MEDLINE 92190628

PUBMED 1799696

COMMENT On Feb 8, 2002 this sequence version replaced gi:247416.

FEATURES

source

1..468

/organism="Pisum sativum"

/strain="Alaska"

/db\_xref="taxon:3888"

/tissue\_type="pod tissue treated with Fusarium solani conidia"

/dev\_stage="immature"

1..468

/gene="DRR230-a"

78..296

/gene="DRR230-a"

/function="unknown"

/standard\_name="pathogenesis related protein"

/note="p1230"

/codon\_start=1

/evidence=experimental

/product="disease resistance response protein"

/protein\_id="AAV9117.1"

/db\_xref="GI:169074"

/translation="MEKSLACISFLLLVFAOEIVSEANTCENLAGSKVCFGGCDRHCRFOEGALISGRCDRDFRCWCTKNC"

159..293

/gene="p1230"

/gene="DRR230-a"

/product="disease resistance response protein"

/function="unknown"

/note="determined by in vitro cleavage with microsomal membranes"

/evidence=experimental

BASE COUNT 153 a 88 c 84 g 143 t

ORIGIN

Alignment Scores:

Pred. No.: 4,34e-16 Length: 468

Score: 214.00 Matches: 33

Percent Similarity: 81.82% Conservative: 3

Best Local Similarity: 75.00% Mismatches: 8

Query Match: 77.82% Indels: 0

DB: 8 Gaps: 0

US-10-010-731-2 (1-45) x PEADRR230A (1-468)

QY 2 ThTCysGluAsnLeuAlaAspLysTYrArgLYProCysPheSerGlyCysAspThrHis 21

Db 162 ACATGTGAGAAATTTGGCTGTCATATAAGGAGATAGCTTCGGTGATGTGACCGGCAC 221

QY 22 CysTThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTPCyS 41

Db 222 TGTAGAACACAGAGGCGCAATTAAGCGGAGATGACGATGACTTCCTGTGGTGC 281

QY 42 ThrLysArgCys 45

Db 282 ACTAAAAACTGT 293

RESULT 4

LOCUS PSP1230 468 bp mRNA linear PLN 09-AUG-2002

DEFINITION P.sativum p1230 mRNA.

ACCESSION X52225

VERSION X52225.1 GI:22208748

KEYWORDS secreted protein.

SOURCE pea.

ORGANISM Pisum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

REFERENCE 1

AUTHORS Chiang, C.C. and Hadwiger, L.A.

TITLE The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins

JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)

MEDLINE 92190628

PUBMED 1799696

COMMENT Submitted (03-AUG-1990) Chiang C., Washington State University, Dept. of Plant Pathology, Pullman, WA 99164-6430, USA

FEATURES

source

1..468

/organism="Pisum sativum"

/db\_xref="taxon:3888"

/tissue\_type="endocarp"

1..468

/gene="p1230"

78..296

/gene="p1230"

/function="unknown"

/standard\_name="pathogenesis related protein"

/note="p1230"

/codon\_start=1

/protein\_id="CAA36474.1"

/db\_xref="GI:22208749"

/translation="MEKSLACISFLLLVFAOEIVSEANTCENLAGSKVCFGGCDRHCRFOEGALISGRCDRDFRCWCTKNC"

159..293

/gene="p1230"

/gene="p1230"

/product="unnamed"

BASE COUNT 153 a 88 c 84 g 143 t

ORIGIN

Alignment Scores:

Pred. No.: 4,34e-16 Length: 468

Score: 214.00 Matches: 33

Percent Similarity: 81.82% Conservative: 3

Best Local Similarity: 75.00% Mismatches: 8

Query Match: 77.82% Indels: 0

DB: 8 Gaps: 0

US-10-010-731-2 (1-45) x PSP1230 (1-468)

QY 2 ThTCysGluAsnLeuAlaAspLysTYrArgLYProCysPheSerGlyCysAspThrHis 21

Db 162 ACATGTGAGAAATTTGGCTGTCATATAAGGAGATAGCTTCGGTGATGTGACCGGCAC 221

QY 22 CysTThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTPCyS 41

Db 222 TGTAGAACACAGAGGCGCAATTAAGCGGAGATGACGATGACTTCCTGTGGTGC 281

QY 42 ThrLysArgCys 45

Db 282 ACTAAAAACTGT 293

RESULT 5

LOCUS AX252303 494 bp DNA linear PAT 05-OCT-2001

DEFINITION Sequence 5 from Patent WO016887.

ACCESSION AX252303

VERSION AX252303.1 GI:15985643

KEYWORDS soybean.

## ORGANISM

Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine

## REFERENCE

1 (bases 1 to 494)  
Jung, R. and Kinney, A. J.  
Hypoallergenic transgenic soybeans  
Patent: WO 0168887-A 5 20-SEP-2001;  
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED  
INTERNATIONAL, INC. (US)

## FEATURES

Source  
Location/Qualifiers  
1..494  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
BASE COUNT 153 a 97 c 103 g 134 t 7 others  
ORIGIN

## Alignment Scores:

Pred. No.: 3.87e-15 Length: 494  
Score: 206.00 Matches: 33  
Percent Similarity: 78.72% Conservative: 4  
Best Local Similarity: 70.21% Mismatches: 8  
Query Match: 74.91% Indels: 2  
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x AX252303 (1-494)

OY 1 ArgThrCysGluSlnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18  
:::|||||  
DB 130 AACACTTGGCAGAACCTGGCTGATACATACAGGGGGTCCAGCTTCACACTGCACCTGC 189  
19 AspThrHisCysThrThrLysGluAsnAlaValSerClyArgCysArgAspAspPheArg 38  
||| |||||  
DB 190 GATGATCACACGCAGAACAAAGACACTTCTCAGAGCGCAGATGCGACGATTTTCGG 249  
OY 39 CysTrpCysThrLysArgCys 45  
|||||  
DB 250 TGTGGTGACACCAAAACTGT 270

## RESULT 6

AB020613 496 bp mRNA linear PLN 05-JAN-2002  
LOCUS  
DEFINITION Vigna radiata mRNA for PDF1, complete cds.  
ACCESSION AB020613  
VERSION AB020613.1 GI:18146787  
KEYWORDS  
SOURCE  
Vigna radiata (strain:B20F5 9-3-2-2) immature seed cDNA to mRNA,  
clone\_lib:B20 clone:pdf-1.  
Vigna radiata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Vigna.

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Vigna.

## REFERENCE

1  
Ishimoto, M. and Kaga, A.  
Mungbean defensin  
Published only in Database (2002)  
2 (bases 1 to 496)

## JOURNAL

1  
Ishimoto, M. and Kaga, A.  
Direct Submission  
Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National  
Agricultural Experiment Station, Laboratory of Plant Biotechnology;  
6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan  
(E-mail:ishimoto@cgk.affrc.go.jp, Tel:+81-849-234100(ex.231),  
Fax:+81-849-247893)

## JOURNAL

1  
Ishimoto, M. and Kaga, A.  
Direct Submission  
Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National  
Agricultural Experiment Station, Laboratory of Plant Biotechnology;  
6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan  
(E-mail:ishimoto@cgk.affrc.go.jp, Tel:+81-849-234100(ex.231),  
Fax:+81-849-247893)

## FEATURES

Source  
Location/Qualifiers  
1..496  
/organism="Vigna radiata"  
/strain="B20F5 9-3-2-2"  
/db\_xref="taxon:157791"  
/clone="pdf-1"  
/tissue\_type="immature seed"

## gene

## CDS

/clone\_lib="B20"  
1..496  
/gene="pdf1"  
46..273  
/gene="pdf1"  
/codon\_start=1  
/product="PDF1"  
/protein\_id="BAB82453.1"  
/db\_xref="GI:18146788"  
/translation="MEKSLAGICPLIVLFVAQEVMTQEAKEKTCENLNTYRGPCT  
TGSCDDHCKKEHLRSGRCDPRCMTNRNC"  
polyA\_site  
496  
/gene="pdf1"  
/note="17 a nucleotides"  
BASE COUNT 148 a 104 c 106 g 138 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2.52e-14 Length: 496  
Score: 199.00 Matches: 32  
Percent Similarity: 78.72% Conservative: 5  
Best Local Similarity: 68.09% Mismatches: 8  
Query Match: 72.36% Indels: 2  
DB: 8 Gaps: 1

US-10-010-731-2 (1-45) x AB020613 (1-496)

OY 1 ArgThrCysGluSlnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18  
:::|||||  
DB 130 AACACTTGGCAGAACCTGGCGAATACATACAGGGGGTCCAGCTTCACACTGCACCTGC 189  
19 AspThrHisCysThrThrLysGluAsnAlaValSerClyArgCysArgAspAspPheArg 38  
||| |||||  
DB 190 GATGATCACACGCAGAACAAAGACACTTAGAGAGTGGCGAGTGCAGGACGATTTCCGG 249  
OY 39 CysTrpCysThrLysArgCys 45  
|||||  
DB 250 TGTGGTGACACTGAAACTGT 270

## RESULT 7

VUSTORED 459 bp mRNA linear PLN 12-SEP-1993  
LOCUS  
DEFINITION Vigna unguiculata cDNA for stored cotyledon mRNA.  
ACCESSION X16877  
VERSION X16877.1 GI:22075  
KEYWORDS  
SOURCE  
Vigna radiata.  
Vigna radiata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Vigna.

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Vigna.

## REFERENCE

1 (bases 1 to 459)  
Yamauchi, D.  
Direct Submission  
Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo  
Metropolitan University, Fukazawa 2-1, Setagaya-ku, Tokyo 158,  
Japan

## JOURNAL

2 (bases 1 to 459)  
Ishibashi, N., Yamauchi, D. and Minamikawa, T.  
Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide  
sequence of cloned cDNA for a stored mRNA and induction of its  
synthesis by precocious germination  
Plant Mol. Biol. 15 (1), 59-64 (1990)

## JOURNAL

1  
Ishibashi, N., Yamauchi, D. and Minamikawa, T.  
Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide  
sequence of cloned cDNA for a stored mRNA and induction of its  
synthesis by precocious germination  
Plant Mol. Biol. 15 (1), 59-64 (1990)

## FEATURES

Source  
Location/Qualifiers  
1..459  
/organism="Vigna radiata"  
/db\_xref="taxon:157791"  
/clone="pSAS10"  
/tissue\_type="cotyledon"  
/clone\_lib="lambda gt10"

CDS

/dev\_stage="seed"  
14..241  
/note="PSAS10 ORF"  
/codon\_start=1  
/protein\_id="CA34760.1"  
/db\_xref="GI:22076"  
/translation="MEKSIAGICFLFLVFAVQAEVVOSEAKTCENLVDTYRGPCFT  
TGSCDHCNKKEHLISGRCDYRCWCTNC"

BASE COUNT 136 a 91 c 99 g 133 t

ORIGIN

Alignment Scores:  
Pred. No.: 3.98e-14 Length: 459  
Score: 197.00 Matches: 31  
Percent Similarity: 76.60% Conservative: 5  
Best Local Similarity: 65.96% Mismatches: 9  
Query Match: 71.64% Indels: 2  
DB: 8 Gaps: 1

US-10-010-731-2 (1-45) x VUSTORED (1-459)

OY 1 ArgThhCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18  
:::|||||  
98 AAGACTTGGCAGAACCTTGTGATACATGAGGGTCCGCTTCACACCTGGAGCTGC 157

DB 19 AspThhHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38  
||| ||||| |||||  
158 GATGATCCTGTCAGAACACAAAGACACTTGTGATGAGGAGTGCGATGATGTCGG 217

OY 39 CysTrpCysThrLysArgCys 45  
|||||  
218 TGTGTGTCACACGAAACTGT 238

DB

RESULT 8

LOCUS A27063 141 bp DNA linear PAT 12-JUN-1995

DEFINITION L. clocera AFP sequence.

ACCESSION A27063

VERSION A27063.1 GI:1247357

KEYWORDS

SOURCE Lathyrus clocera.

ORGANISM Lathyrus clocera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaceae;  
Lathyrus.

FEATURES  
source Location/Qualifiers  
1..141  
/organism="Lathyrus clocera"  
/db\_xref="taxon:3856"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:  
Pred. No.: 2.85e-11 Length: 141  
Score: 168.00 Matches: 25  
Percent Similarity: 70.21% Conservative: 8  
Best Local Similarity: 53.19% Mismatches: 12  
Query Match: 61.09% Indels: 2  
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x A27063 (1-141)

OY 1 ArgThhCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18  
:::|||||  
1 AAGACTTGGCAGAACCTTGTGATGAGGAGCAGATTCAGATGGAACCTGC 60

DB 19 AspThhHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38  
::: ||||| |||||  
61 AAGACATTTGCAAGAACAGACATCTTTCTTGGAAGATGACAGATGATTCNNN 120

OY 39 CysTrpCysThrLysArgCys 45

DB 121 TGCTGTGCACATGAAACTGC 141  
|||||  
RESULT 9

LOCUS A39547 141 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 35 from Patent WO9416076.

ACCESSION A39547

VERSION A39547.1 GI:2295840

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 141)  
Dubock, A.C., Powell, K. A. and Rees, S. B.  
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS  
TITLE Patent: WO 9416076-A 35 21-JUL-1994;  
JOURNAL ZENECA LTD (GB)  
COMMENT Other publication AU 5820494 940815.  
FEATURES  
source Location/Qualifiers  
1..141  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:  
Pred. No.: 2.85e-11 Length: 141  
Score: 168.00 Matches: 25  
Percent Similarity: 70.21% Conservative: 8  
Best Local Similarity: 53.19% Mismatches: 12  
Query Match: 61.09% Indels: 2  
DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x A39547 (1-141)

OY 1 ArgThhCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18  
:::|||||  
1 AAGACTTGGCAGAACCTTGTGATGAGGAGCAGATTCAGATGGAACCTGC 60

DB 19 AspThhHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38  
::: ||||| |||||  
61 AAGACATTTGCAAGAACAGACATCTTTCTTGGAAGATGACAGATGATTCNNN 120

OY 39 CysTrpCysThrLysArgCys 45  
|||||  
121 TGCTGTGCACATGAAACTGC 141

DB

RESULT 10

LOCUS AR050147 141 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 35 from patent US 5824869.

ACCESSION AR050147

VERSION AR050147.1 GI:5972139

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 141)  
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,  
Terras, F.R.G. and Vanderleyden, J.,  
TITLE Bioicidal proteins  
JOURNAL Patent: US 5824869-A 35 20-OCT-1998;  
FEATURES  
source Location/Qualifiers  
1..141  
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

ORIGIN

Alignment Scores:  
Pred. No.: 2.85e-11 Length: 141  
Score: 168.00 Matches: 25  
Percent Similarity: 70.21% Conservative: 8

Best Local Similarity: 53.19% Mismatches: 12  
 Query Match: 61.09% Indels: 2  
 DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x AR050147 (1-141)

OY 1 ArgThhCysGluAsnLeuAlaAspLysTYrArgGlyProCysPhe-----SerGlyCys 18  
 1 AAGACTTGGCAGAACCTTCTTGGAACTTTCAGAGGACCATTCATTCAGATGGAACCTGC 60  
 Db

OY 19 AspThhHisCysThrThrLysGluAsnAlaValSerGlyYrGlyCysArgAspAspPheArg 38  
 61 AACAGCATTGGCAAGAACCAAGACATCTTCTTGGAGATGACAGATGATTCNNN 120  
 Db

OY 39 CysTrpCysThrLysArgCys 45  
 121 TGCTGTGTCACCTAGAAACTGC 141  
 Db

RESULT 11  
 ARI30266 141 bp DNA Linear PAT 16-MAY-2001  
 LOCUS Sequence 35 from patent US 6187904.  
 ARI30266  
 ACCESSION ARI30266.1 GI:14118163  
 VERSION  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM

REFERENCE 1 (bases 1 to 141)  
 Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
 Terras,F.R.G. and Vanderleyden,J.  
 TITLE Bioicidal proteins  
 JOURNAL Patent: US 6187904-A 35 13-FEB-2001.  
 FEATURES location/Qualifiers  
 source 1..141  
 /organism="unknown"  
 BASE COUNT 43 a 30 c 32 g 33 t 3 others  
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 Score: 168.00 Matches: 25  
 Percent Similarity: 70.21% Conservative: 8  
 Best Local Similarity: 53.19% Mismatches: 12  
 Query Match: 61.09% Indels: 2  
 DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x ARI30266 (1-141)

OY 1 ArgThhCysGluAsnLeuAlaAspLysTYrArgGlyProCysPhe-----SerGlyCys 18  
 1 AAGACTTGGCAGAACCTTCTTGGAACTTTCAGAGGACCATTCATTCAGATGGAACCTGC 60  
 Db

OY 19 AspThhHisCysThrThrLysGluAsnAlaValSerGlyYrGlyCysArgAspAspPheArg 38  
 61 AACAGCATTGGCAAGAACCAAGACATCTTCTTGGAGATGACAGATGATTCNNN 120  
 Db

OY 39 CysTrpCysThrLysArgCys 45  
 121 TGCTGTGTCACCTAGAAACTGC 141  
 Db

RESULT 12  
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 LOCUS Sequence 35 from patent US 5538525.  
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 ACCESSION 123722.1 GI:1603592  
 VERSION  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM

REFERENCE 1 (bases 1 to 141)  
 Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
 AUTHORS

Terras,F.R.G. and Vanderleyden,J.  
 TITLE Bioicidal proteins  
 JOURNAL Patent: US 5538525-A 35 23-JUL-1996.  
 FEATURES location/Qualifiers  
 source 1..141  
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 BASE COUNT 43 a 30 c 32 g 33 t 3 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2.85e-11 Length: 141  
 Score: 168.00 Matches: 25  
 Percent Similarity: 70.21% Conservative: 8  
 Best Local Similarity: 53.19% Mismatches: 12  
 Query Match: 61.09% Indels: 2  
 DB: 6 Gaps: 1

US-10-010-731-2 (1-45) x 123722 (1-141)

OY 1 ArgThhCysGluAsnLeuAlaAspLysTYrArgGlyProCysPhe-----SerGlyCys 18  
 1 AAGACTTGGCAGAACCTTCTTGGAACTTTCAGAGGACCATTCATTCAGATGGAACCTGC 60  
 Db

OY 19 AspThhHisCysThrThrLysGluAsnAlaValSerGlyYrGlyCysArgAspAspPheArg 38  
 61 AACAGCATTGGCAAGAACCAAGACATCTTCTTGGAGATGACAGATGATTCNNN 120  
 Db

OY 39 CysTrpCysThrLysArgCys 45  
 121 TGCTGTGTCACCTAGAAACTGC 141  
 Db

RESULT 13  
 PEARRR230B 456 bp mRNA Linear PLN 11-FEB-2002  
 LOCUS  
 DEFINITION Pisum sativum disease resistance response protein 39 (DRR230-b)  
 mRNA, complete cds.  
 L01579.1 GI:169075  
 ACCESSION L01579.1 GI:169075  
 VERSION  
 KEYWORDS cysteine-rich protein; disease resistance response protein 39;  
 pathogenesis-related protein.  
 SOURCE Pisum sativum (strain Alaska) cDNA to mRNA.  
 ORGANISM Pisum sativum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;  
 Pisum.

REFERENCE 1 (bases 1 to 456)  
 Chiang,C.C. and Hadwiger,L.A.  
 TITLE The Fusarium solani-induced expression of a pea gene family  
 encoding high cysteine content proteins  
 JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)  
 MEDLINE 92190628  
 PUBMED 1799696  
 COMMENT On Feb 8, 2002 this sequence version replaced gi:247414.  
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 /strain="Alaska"  
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 69..293  
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 CDS



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Score:             141.50         Matches:     24
Percent Similarity: 69.57%        Conservative: 8
Best local Similarity: 52.17%      Mismatches:  11
Query Match:       51.45%         Indels:     3
DB:                8              Gaps:       2
US-10-010-731-2 (1-45) x PEADRR230B (1-456)

Qy      2   ThrCysgluaInLeuAlaAspLysTyrArgIlyProCysPhe-----SerGIYcysasp 19
Db      156 ACTGTGAGACATTGGCGTGATACACTACAGGGGAGATATGCTTCACAGAATGCTAGCTGAT 215
Qy      20   ThrHisCysThrThrLysGLuaSnAlaValserGIYArGcysArgAspAspPheArgCys 39
Db      216 GATCACGTGCAGAAACAAGCCGCACTTATCATGTCAGTCGCATC---GACTGGAAATGT 272
Qy      40   TrpCysThrIlyArgCys 45
Db      273 TTTCTGCACCTCAAACCTGT 290

RESULT 14
LOCUS      PSP139                      456 bp      mRNA      linear      PLN 09-AUG-2002
DEFINITION P. sativum p139 mRNA.
ACCESSION  X52224
VERSION    X52224.1 GI:22208744
KEYWORDS   secreted protein.
SOURCE     pea.
ORGANISM   Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
            Pisum.
REFERENCE   1
AUTHORS    Chiang,C.C. and Hadwiger,L.A.
TITLE      The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
JOURNAL    Mol. Plant Microbe Interact. 4 (4), 324-331 (1991).
MEDLINE    92190628
REFERENCE   2 (bases 1 to 456)
AUTHORS    Chiang,C.
TITLE      Direct Submission
JOURNAL    Submitted (03-AUG-1990) Chiang C., Washington State University,
            Dept. of Plant Pathology, Pullman, WA 99164-6430, USA
FEATURES
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/translation="MHDIETYHNSQSRIOHTGAVOILHIIVEFIHIMSFIHLILSLR  
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BASE COUNT 120 a 78 c 64 g 118 t  
ORIGIN

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Pred. No.:	1.02e-07	Length:	380
Score:	141.00	Matches:	22
Percent Similarity:	67.50%	Conservative:	5
Best Local Similarity:	55.00%	Mismatches:	11
Query Match:	51.27%	Indels:	2
DB:	8	Gaps:	1

US-10-010-731-2 (1-45) x AB049718 (1-380)

QY 8 AsplysTyrrArgGlyProCysPhe-----SerGlyCysAspThrHisCysThrTrlys 25  
DB 368 AATAAACAACACTGGGACCATGCATCCAGATGTACTGCACAACAACATTGCAGCAACAAC 309  
QY 26 GluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTrpCysThrLysArgCys 45  
DB 308 GAGCACATACCTAGAGTGGAGGATGCAGGATGATTTCCCTGCTGCTGCTGCACTCGAAGACTGT 249

Search completed: June 21, 2003, 07:19:17  
Job time : 1795.65 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 05:36:29 ; Search time 164.647 Seconds  
(without alignments)  
615.498 Million cell updates/sec

Title: US-10-010-731-2

Perfect score: 275  
Sequence: 1 RTCEMLADKYRGPCFSGCDT.....ENAVSGRCRDRCFCWCTKRC 45

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cogn2.1/USPFC.spool/US10010731/runat.17062003.095704.28153/app.query.fasta.1.398  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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Database :  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	275	100.0	250	19	AAV39187	Alfalfa plant anti
2	275	100.0	490	19	AAV39186	Antifungal polypep
3	275	100.0	507	19	AAV39195	Antifungal polypep
4	241	87.6	327	19	AAV39194	Antifungal polypep
5	231	84.0	200	19	AAV39190	Antifungal polypep
6	214	77.8	468	21	AAZ49412	Pea defensin prote
7	206	74.9	494	22	AAAD17530	Soybean Gly m2 pro
8	185	67.3	293	19	AAV39191	Antifungal polypep
9	168	61.1	141	15	AAO70126	Antimicrobial Lc-A
10	158.5	57.6	138	14	AAO38648	Encodes antifungal
11	91	33.1	487	21	AAAC34773	Arabidopsis thalia
12	91	33.1	552	21	AAA78455	Plant SDR polynuc
13	91	33.1	552	21	AAA78544	Plant SDR polynuc
14	88	32.0	489	21	AAAC44316	Arabidopsis thalia
15	88	32.0	526	21	AAAC34077	Arabidopsis thalia
16	87	31.6	510	21	AAAC45669	Arabidopsis thalia
17	87	31.6	512	21	AAAC32882	Arabidopsis thalia
18	81	29.5	47	19	AAV39197	Antifungal polypep
19	80.5	29.3	823	23	ABU16863	Drosophila melanog
20	80.5	29.3	2823	23	ABU16862	Drosophila melanog
21	80	29.1	458	24	ABN94581	Gene #1079 used to
22	80	29.1	1546	24	ABO54166	Human ovarian anti
23	79.5	28.9	693	15	AAO58991	Diospyros texana a
24	78.5	28.5	627	15	AAO58992	Diospyros texana a
25	78	28.4	465	21	AAAC34026	Arabidopsis thalia
26	78	28.4	520	21	AAAC35542	Arabidopsis thalia
27	78	28.4	597	21	AAAC40605	Arabidopsis thalia
28	76.5	27.8	363	15	AAO70067	Sequence encoding
29	76.5	27.8	492	15	AAO70064	Sequence encoding
30	73.5	26.7	499	22	AAAS4398	Plant defensin par
31	73.5	26.7	517	22	AAAS4399	Plant defensin cod
32	72.5	26.4	167	20	AAAX15805	CDNA encoding the
33	72.5	26.4	236	20	AAAX15806	CDNA encoding the
34	72.5	26.4	376	23	ABU16859	Drosophila melanog
35	72.5	26.4	488	20	AAAX15804	CDNA encoding dtos
36	72.5	26.4	2376	23	ABU16858	Drosophila melanog
37	72	26.2	147	14	AAO38649	Encodes antifungal
38	72	26.2	147	15	AAO70127	Antimicrobial Ct-A
39	71.5	26.0	219	23	ABU16865	Drosophila melanog
40	71.5	26.0	2219	23	ABU16864	Drosophila melanog
41	71.5	26.0	2784	23	ABU17936	Drosophila melanog
42	71.5	26.0	11043	23	ABU28123	Drosophila melanog
43	70.5	25.6	550	21	AAZ48826	Human delta1 codin
44	70.5	25.6	1980	18	AAAT59454	H-Delta-1 contig c
45	70.5	25.6	2663	18	AAAT70174	Proliferation and

## ALIGNMENTS

RESULT 1	AAV39187	standard; DNA; 250 BP.
ID	AAV39187	
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AC		
XX		
DT	25-SEP-1998 (first entry)	
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DE	Alfalfa plant antifungal polypeptide AlfAlfP1 encoding DNA.	
XX		
KW	Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;	
KW	plant pathogenic fungus; AlfAlfP1; AlfAlfP2; ds.	
XX		
OS	Medicago sativa.	
XX		
FH	key	Location/Qualifiers
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 PN 18-JUN-1998.  
 PD 11-DEC-1997: 97MO-US22662.  
 XX 13-DEC-1996: 96US-0766355.  
 XX (MONS ) MONSANTO CO.  
 PA Haktim S, Liang J, Rosenberger CA, Shah DM, Wu YS;  
 PI WPI: 1998-348537/30.  
 DR P-PSDB; AAW61964.  
 XX  
 PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)  
 PT - used to control plant pathogenic fungi and to produce transformed  
 PT plants with increased fungal resistance  
 PS  
 PS Claim 3: Page 78; 97pp: English.  
 XX  
 CC This DNA encodes an antifungal polypeptide, AlfALFPI isolated from  
 CC alfalfa plants (Medicago). The polypeptides AlfALFPI and AlfALFP2 are  
 CC useful to control plant fungi, especially pathogenic fungi, by  
 CC transforming plant cells with a vector comprising sequences encoding  
 CC AlfALFPI or AlfALFP2 to allow expression of antifungally effective amounts  
 CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,  
 CC cotton and especially potato. Micro-organisms may also be transformed  
 CC to produce the polypeptides, and applied to plants to control plant  
 CC fungi. The polypeptides can also be included with a suitable solvent in  
 CC antifungal compositions and these can be administered to plants to  
 CC control plant fungi. Such compositions and genetically engineered plants  
 CC may also contain additional molecules e.g. the compositions can contain  
 CC other antifungal agents or the plants contain DNA encoding insecticidal  
 CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful  
 CC to prepare antibodies useful to detect polypeptides or isolate other  
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
 CC to produce polypeptides and transgenic plants and as probes or primers in  
 CC nucleic acid hybridisation e.g. to detect complementary sequences in  
 CC samples, and to prepare mutants or isolate similar sequences from related  
 CC species.  
 CC  
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 SQ Sequence 250 BP: 73 A; 48 C; 64 G; 65 T; 0 other:  
 Alignment Scores:  
 Pred. No.: 1,78e-25 Length: 250  
 Score: 275.00 Matches: 45  
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 Db 105 AGAACATGTGAGATTTGGCAGATAATATAGGGGACCAATGCTTAGTGGTTGTGACACT 164  
 QY 21 HisCysThrThylsGluAsnAlaValSerGlyAryCysArgAspAspPheArgCysTrp 40  
 Db 165 CACTGCACCAACCAAGAGACGCTAGTGAAGCTGTAGGACGACCTCCCTCTCG 224  
 QY 41 CysThrLysArgCys 45  
 Db 225 TGTACTAAAGATGT 239  
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 ID AAV39186 standard; DNA: 490 BP.  
 XX  
 AC AAV39186;

XX 01-OCT-1998 (first entry)  
 DT Antifungal polypeptide AlfALFPI encoding cDNA.  
 XX  
 DE Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance;  
 XX plant pathogenic fungus; AlfALFPI; AlfALFP2; ss.  
 KW  
 KW Medicago sativa.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 75..293  
 FT /\*tag= a  
 FT /transl\_except= (pos:129..131, aa:Glu)  
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 FT sig\_peptide 75..155  
 FT /\*tag= b  
 FT mat\_peptide 156..290  
 FT /\*tag= c  
 FT  
 PN MO9826083-A1.  
 PD 18-JUN-1998.  
 PD 11-DEC-1997: 97MO-US22662.  
 PF 13-DEC-1996: 96US-0766355.  
 PR (MONS ) MONSANTO CO.  
 PA Haktim S, Liang J, Rosenberger CA, Shah DM, Wu YS;  
 PI WPI: 1998-348537/30.  
 DR P-PSDB; AAW61964.  
 XX  
 PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)  
 PT - used to control plant pathogenic fungi and to produce transformed  
 PT plants with increased fungal resistance  
 PS  
 PS Claim 5: Fig 1: 97pp: English.  
 XX  
 CC This cDNA encodes an antifungal polypeptide, AlfALFPI isolated from  
 CC alfalfa plants (Medicago). The polypeptides AlfALFPI and AlfALFP2 are  
 CC useful to control plant fungi, especially pathogenic fungi, by  
 CC transforming plant cells with a vector comprising sequences encoding  
 CC AlfALFPI or AlfALFP2 to allow expression of antifungally effective amounts  
 CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,  
 CC cotton and especially potato. Micro-organisms may also be transformed  
 CC to produce the polypeptides, and applied to plants to control plant  
 CC fungi. The polypeptides can also be included with a suitable solvent in  
 CC antifungal compositions and these can be administered to plants to  
 CC control plant fungi. Such compositions and genetically engineered plants  
 CC may also contain additional molecules e.g. the compositions can contain  
 CC other antifungal agents or the plants contain DNA encoding insecticidal  
 CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful  
 CC to prepare antibodies useful to detect polypeptides or isolate other  
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
 CC to produce polypeptides and transgenic plants and as probes or primers in  
 CC nucleic acid hybridisation e.g. to detect complementary sequences in  
 CC samples, and to prepare mutants or isolate similar sequences from related  
 CC species.  
 CC  
 XX  
 SQ Sequence 490 BP: 182 A; 85 C; 85 G; 136 T; 2 other:  
 Alignment Scores:  
 Pred. No.: 4.07e-25 Length: 490  
 Score: 275.00 Matches: 45  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0  
 US-10-010-731-2 (1-45) x AAV39186 (1-490)

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OY      1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
DB      156 AGAACATGTCAGATTGGCAGATTAATATAGGGGACCATGCTTTAGTGGTGGACACT 215
OY      21 HisCysThrThrlYsgLlAsnAlaValSerGlyAArgCysAArgAspApeAArgCysTTP 40
DB      216 CACTGCACACCAAGAGACGAGTGTAGTGAAGGTGTAGGACGACACTTCCGCTGTGG 275
OY      41 CysThrLysAArgCys 45
DB      276 TGTACTAAAGATGT 290

RESULT 3
AAV39195
ID      AAV39195 standard; DNA: 507 BP.
AC      AAV39195;
DT      25-SEP-1998 (first entry)
XX      Antifungal polypeptide AlfAP1 mature sequence encoding DNA.
DE      Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance:
KM      plant pathogenic fungus; AlfAP1; AlfAP2; ds.
XX      Medicago sativa.
OS      Medicago sativa.
FH      Key
FT      Location/Qualifiers
FT      173..310
FT      /*lag= a
FT      /*product= "mature AlfAP1"
XX      WO9826083-A1.
XX      18-JUN-1998.
XX      11-DEC-1997; 97WO-US22662.
XX      13-DEC-1996; 96US-0766355.
XX      (MONS ) MONSANTO CO.
XX      Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
PI      WPI: 1998-348537/30.
DR      P-PSDB; AAW61964.
XX      Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT      - used to control plant pathogenic fungi and to produce transformed
PT      plants with increased fungal resistance
XX      Claim 5; Page 77; 97pp; English.
XX      This DNA encodes an antifungal polypeptide, AlfAP1 isolated from
CC      alfalfa plants (Medicago). The polypeptides AlfAP1 and AlfAP2 are
CC      useful to control plant fungi, especially pathogenic fungi, by
CC      transforming plant cells with a vector comprising sequences encoding
CC      AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts
CC      of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC      cotton and especially potato. Micro-organisms may also be transformed
CC      to produce the polypeptides, and applied to plants to control plant
CC      fungi. The polypeptides can also be included with a suitable solvent in
CC      antifungal compositions and these can be administered to plants to
CC      control plant fungi. Such compositions and genetically engineered plants
CC      may also contain additional molecules e.g. the compositions can contain
CC      other antifungal agents or the plants contain DNA encoding insecticidal
CC      (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC      to prepare antibodies useful to detect polypeptides or isolate other
CC      alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC      to produce polypeptides and transgenic plants and as probes or primers in
CC      nucleic acid hybridisation e.g. to detect complementary sequences in
CC      samples, and to prepare mutants or isolate similar sequences from related
```

```
CC      species.
XX      SQ      Sequence 507 BP: 181 A; 85 C; 102 G; 136 T; 3 other:
Alignment Scores:
Pred. No.: 4.25e-25
Score: 275.00
Percent Similarity: 100.00%
Best local Similarity: 100.00%
Query Match: 100.00%
DB: 19
Gaps: 0
US-10-010-731-2 (1-45) x AAV39195 (1-507)
OY      1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20
DB      173 AGAACATGTCAGATTGGCAGATTAATATAGGGGACCATGCTTTAGTGGTGGACACT 232
OY      21 HisCysThrThrlYsgLlAsnAlaValSerGlyAArgCysAArgAspApeAArgCysTTP 40
DB      233 CACTGCACACCAAGAGACGAGTGTAGTGAAGGTGTAGGACGACACTTCCGCTGTGG 292
OY      41 CysThrLysAArgCys 45
DB      293 TGTACTAAAGATGT 307

RESULT 4
AAV39194
ID      AAV39194 standard; DNA: 327 BP.
AC      AAV39194;
DT      25-SEP-1998 (first entry)
XX      Antifungal polypeptide AlfAP2 3' region.
DE      Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance:
KM      plant pathogenic fungus; AlfAP1; AlfAP2; ds.
XX      Medicago sativa.
OS      Medicago sativa.
FH      Key
FT      Location/Qualifiers
FT      173..310
FT      /*lag= a
FT      /*product= "mature AlfAP1"
XX      WO9826083-A1.
XX      18-JUN-1998.
XX      11-DEC-1997; 97WO-US22662.
XX      13-DEC-1996; 96US-0766355.
XX      (MONS ) MONSANTO CO.
XX      Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
PI      WPI: 1998-348537/30.
DR      P-PSDB; AAW61964.
XX      Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT      - used to control plant pathogenic fungi and to produce transformed
PT      plants with increased fungal resistance
XX      Claim 18; Page 77; 97pp; English.
XX      This sequence represents the 3' region of the DNA encoding an antifungal
CC      polypeptide, AlfAP2 isolated from alfalfa plants (Medicago). The
CC      polypeptides AlfAP1 and AlfAP2 are useful to control plant fungi,
CC      especially pathogenic fungi, by transforming plant cells with a vector
CC      comprising sequences encoding AlfAP1 or AlfAP2 to allow expression of
CC      antifungally effective amounts of the polypeptide. Such transformed
CC      plants may be e.g. apple, wheat, cotton and especially potato.
CC      Micro-organisms may also be transformed to produce the polypeptides, and
CC      applied to plants to control plant fungi. The polypeptides can also be
CC      included with a suitable solvent in antifungal compositions and these can
CC      be administered to plants to control plant fungi. Such compositions and
CC      genetically engineered plants may also contain additional molecules e.g.
```

CC the compositions can contain other antifungal agents or the plants  
CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)  
CC proteins. The polypeptides are also useful to prepare antibodies useful  
CC to detect polypeptides or isolate other alfalfa plant antifungal protein  
CC antigens. The nucleic acids are useful to produce polypeptides and  
CC transgenic plants and as probes or primers in nucleic acid hybridisation  
CC e.g. to detect complementary sequences in samples, and to prepare mutants  
CC or isolate similar sequences from related species.

XX  
SQ Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other:

Alignment Scores:

Pred. No.:	4.02e-21	Length:	327
Score:	241.00	Matches:	41.
Percent Similarity:	97.62%	Conservative:	0
Best Local Similarity:	97.62%	Mismatches:	1
Query Match:	87.64%	Indels:	0
DB:	19	Gaps:	0

US-10-010-731-2 (1-45) x AAV39194 (1-327)

OY 4 GluasnleuAlaaspLysTYrArgGLyProCysPheSerGlyCysAspThrHisCysThr 23

Db 1 GAGATTTCGGCGATTAAGTATAGGGGACCAATGCTTTAGTGTGTGACACTCAGTCACA 60

OY 24 ThrLysGluAsnAlaValSerGlyArgCysArgAspPheArgCysTrpCysThrLys 43

Db 61 ACCAAGACAGAACCGAGTACTGAGAGGTGTAGGATGACTTTCCTTTAGTGTACTATAA 120

OY 44 ArgCys 45

Db 121 AGATGT 126

RESULT 5  
AAV39190

ID AAV39190 standard; DNA; 200 BP.

XX AAV39190;

DT 25-SEP-1998 (first entry)

XX Antifungal polypeptide AlfaFP2 5' region.

XX Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;

XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.

XX Medicago sativa.

XX WO9826083-A1.

PD 18-JUN-1998.

PF 11-DEC-1997; 97WO-US22662.

PR 13-DEC-1996; 96US-0766355.

XX (MONS ) MONSANTO CO.

PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;

DR WPI; 1998-348537/30.

XX Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)

XX - used to control plant pathogenic fungi and to produce transformed

XX plants with increased fungal resistance

XX Claim 18; Page 75; 97pp; English.

XX This sequence represents the 5' region of the DNA encoding an antifungal

XX polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The

XX polypeptides AlfaFP1 and AlfaFP2 are useful to control plant fungi,

XX especially pathogenic fungi, by transforming plant cells with a vector

XX comprising sequences encoding AlfaFP1 or AlfaFP2 to allow expression of

CC antifungally effective amounts of the polypeptide. Such transformed

CC plants may be e.g. apple, wheat, cotton and especially potato.

CC Micro-organisms may also be transformed to produce the polypeptides, and

CC applied to plants to control plant fungi. The polypeptides can also be

CC included with a suitable solvent in antifungal compositions and these can

CC be administered to plants to control plant fungi. Such compositions and

CC genetically engineered plants may also contain additional molecules e.g.

CC the compositions can contain other antifungal agents or the plants

CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)

CC proteins. The polypeptides are also useful to prepare antibodies useful

CC to detect polypeptides or isolate other alfalfa plant antifungal protein

CC antigens. The nucleic acids are useful to produce polypeptides and

CC transgenic plants and as probes or primers in nucleic acid hybridisation

CC e.g. to detect complementary sequences in samples, and to prepare mutants

CC or isolate similar sequences from related species.

XX  
SQ Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other:

Alignment Scores:

Pred. No.:	3.79e-20	Length:	200
Score:	231.00	Matches:	39
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	84.00%	Indels:	0
DB:	19	Gaps:	0

US-10-010-731-2 (1-45) x AAV39190 (1-200)

OY 1 ArgThrCysGluAsnleuAlaaspLysTYrArgGLyProCysPheSerGlyCysAspThr 20

Db 80 AGAACATGTGATGATTTGGCGAGATTAATATAGGGGACCAATGCTTTAGTGTGTGACACT 139

OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArgCys 39

Db 140 CACTGCACACCAACAGACGAGTGTAGTGAAGGTGTAGGGACCACTTCCCTGC 196

RESULT 6  
AAZ49412

ID AAZ49412 standard; cDNA; 468 BP.

XX AAZ49412;

DT 04-APR-2000 (first entry)

XX Pea Defensin protein Drr230, encoding cDNA.

XX Transgenic plant; disease resistance; DRR206; defensin; Drr230; PR10.1;

XX chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;

XX CamV 35S inducible promoter; T-DNA; bacterial/fungal pathogen;

XX Leptosphaeria maculans; Rhizoctonia solani; Sclerotinia sclerotiorum; ds.

XX Pisum sativum.

XX WO200001824-A2.

PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-CA00608.

PR 03-JUL-1998; 98CA-2242116.

PR 06-JUL-1998; 98US-0091751.

XX (UYMA-) UNIV MANITOBA.

XX Fristensky B, Wang Y;

DR	WPI: 2000-126938/11.	
DR	P-PSDB: AAAY44509.	
XX	Recombinant expression system for expressing DRR206 or defensin, used	
PT	to produce pathogen resistant <i>Brassica napus</i>	
XX		
PS	Claim 11; Fig 9; 39pp; English.	
XX		
CC	The present sequence is the cDNA encoding defensin protein, derived from	
CC	the clone Drr220 of pea. This sequence is strongly induced by bacterial	
CC	and fungal pathogens like, blackleg fungus. This gene is used in a	
CC	recombinant expression system, capable of transforming plants like,	
CC	<i>Canola</i> ( <i>Brassica napus</i> ), under the constitutive control of <i>CaMV 35S</i>	
CC	inducible promoter, responsive to pathogen infections. T-DNA sequence is	
CC	also present, for integration of the expression system into the plant	
CC	genome. Transgenic plants expressing DRR206 and defensin protein,	
CC	inhibited fungal growth in-vitro and are resistant to pathogenic	
CC	infections of <i>Rhizoctonia solani</i> , <i>Leptosphaeria maculans</i> and <i>Sclerotinia</i>	
CC	<i>sclerotiorum</i> .	
XX		
SO	Sequence 468 BP; 153 A; 88 C; 84 G; 143 T; 0 other;	
	Alignment Scores:	
	Pred. NO:	1.38e-17
	Score:	214.00
	Percent Similarity:	81.82%
	Best Local Similarity:	75.00%
	Query Match:	77-82%
	DB:	21
		Gaps: 0
US-10-010-731-2 (1-45) x AA249412 (1-468)		
QY	2 ThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHis 21	
DB	162 ACATGTGAGAAATTGGCTGCTTCATATTAAGGAGATGATCTTCGGTGATGACCGCAC 221	
QY	22 CysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTrpCys 41	
DB	222 TGTGAAGAACCAAGAGGGCGCAATTAGCGGCAGACATCAGAGATGACTTTCCTGTTGGTGC 281	
QY	42 ThrLysArgCys 45	
DB	282 ACTAAAAACTGT 293	
RESULT 7		
ID	AAAD17530	
XX	AAAD17530 standard; cDNA; 494 BP.	
AC	AAAD17530;	
XX		
DT	10-DEC-2001 (first entry)	
XX		
DE	Soybean Gly m2 protein encoding cDNA from clone sls1c.pk027.all.	
XX		
XX	Soybean: allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1;	
KW	soybean vacuolar protein; Gly m 1A; Gly m 1B; RGLY m3; Glycinin G1;	
KW	alabib; food; infant formula; animal feed; coating; salad oil; syrup;	
KW	spraying oil; roasting oil; frying oil; cracker; confectionery product;	
KW	snack food; topping; sauce; batter; breading mixture; baking mix; dough;	
XX	Gly m2 protein; clone sls1c.pk027.all; ss.	
XX		
OS	Glycine max.	
XX		
EH	key	Location/Qualifiers
FT	CDS	46..273
FT		/*lag= a
XX		/product="Soybean Gly m2 protein"
PN	WO200168887-A2.	
XX		
ED	20-SEP-2001.	
XX		
PF	15-MAR-2001; 2001WO-US08254.	

```

XX 16-MAR-2000; 2000US-0189823.
XX
XX (DUP0 ) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Jung R, Kinney AJ;
XX
XX WPI: 2001-582460/65.
XX P-PSDB; AAE10361.
XX
XX Recombinant expression construct to lower allergen (e.g. Gly m Bd 30k)
XX content of a soybean, comprises a nucleic acid fragment encoding the
XX allergen, useful for producing soybean plants which can be used to make
XX soybean products
XX
XX
XX Example 7; Page 51-52; 57pp; English.
XX
XX The patent discloses hypallergenic transgenic soybeans and recombinant
XX expression constructs to lower soybean vacuolar protein, commonly known
XX as P34 (Gly m Bd 30k or Gly m 1) and other allergens such as Gly m 1b,
XX Gly m 1b, rclm m3 or Glycinin G1 (a1ar1b). The allergen content of the
XX soybean is reduced by sense suppression which is accomplished by using
XX the expression construct that comprises a nucleic acid fragment encoding
XX the allergen. The constructs are useful for producing hypallergenic
XX transgenic soybean plants which can be used to make hypallergenic
XX soybean products which can be used in a variety of food (e.g. infant
XX formulas) and animal feed applications. The oil made from seeds of the
XX hypallergenic transgenic soybean plants can be used as ingredients,
XX as coatings, as salad oils, as spraying oils, as roasting oils, and
XX as frying oils. The foods in which the oil may be used include crackers
XX and snack foods, confectionery products, syrups and toppings, sauces,
XX batter and breeding mixtures, baking mixes and doughs. The present
XX sequence is soybean Gly m2 protein encoding cDNA from s1slc.pk027.all
XX clone. This sequence is a minor soybean seed allergen.
XX
XX Sequence 494 BP; 153 A; 97 C; 103 G; 134 T; 7 other;
XX
XX
XX Alignment Scores:
XX Pred. NO.: 1,44e-16 Length: 494
XX Percent Similarity: 206.00 Matches: 33
XX Best Local Similarity: 78.72% Conservative: 4
XX Query Match: 70.21% Mismatches: 8
XX DB: 74.91% Indels: 2
XX Gaps: 1
XX
XX US-10-010-731-2 (1-45) x AAD17530 (1-494)
XX
XX QY 1 ArgThrCysGlnuSnleuAlaSpLyTrhArgGlyProCysPheSer-----GlyCys 18
XX ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 130 AAcACTGGcAGAAcCTGGcTATACATACAGGGcTCCATCTTCACcAGCGAGCTGC 189
XX 19 AspThrHisCysThrThrCysGlnuSnAlaValISerGlyTrhArgCysAspAspPheArg 38
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX Db 190 GATGATCATCAGCGAAGAAAGAGAGCATTGCTCAAGAGGcCATGAGGAGGAGATTTCGC 249
XX 39 CysTrpCysThrLysArgCys 45
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX QY 250 TGTGGTGCGACCAAAACACTGT 270
XX
XX RESULT 8
XX AAV39191
XX ID AAV39191 standard; DNA; 293 BP.
XX
XX AAV39191;
XX
XX 25-SEP-1998 (first entry)
XX
XX Antifungal polypeptide AlfAFP2 coding sequence.
XX
XX Antifungal polypeptide: alfalfa plant; Medicago; fungal resistance;
XX plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX

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OS Medicago sativa.  
XX  
PN MO9826083-A1.  
XX  
PD 18-JUN-1998.  
XX  
PF 11-DEC-1997; 97MO-US22662.  
XX  
PR 13-DEC-1996; 96US-0766355.  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;  
XX  
DR WPI; 1998-348537/30.  
XX  
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)  
PT - used to control plant pathogenic fungi and to produce transformed  
PT plants with increased fungal resistance  
XX  
PS Claim 18; Page 75; 97pp; English.

CC This represents a coding sequence of an antifungal polypeptide, AlfAP2  
CC isolated from alfalfa plants (Medicago). The polypeptides AlfAP1 and  
CC AlfAP2 are useful to control plant fungi, especially pathogenic fungi,  
CC by transforming plant cells with a vector comprising sequences encoding  
CC AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts  
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,  
CC cotton and especially potato. Micro-organisms may also be transformed  
CC to produce the polypeptides, and applied to plants to control plant  
CC fungi. The polypeptides can also be included with a suitable solvent in  
CC antifungal compositions and these can be administered to plants to  
CC control plant fungi. Such compositions and genetically engineered plants  
CC may also contain additional molecules e.g. the compositions can contain  
CC other antifungal agents or the plants contain DNA encoding insecticidal  
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful  
CC to prepare antibodies useful to detect polypeptides or isolate other  
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
CC to produce polypeptides and transgenic plants and as probes or primers in  
CC nucleic acid hybridisation e.g. to detect complementary sequences in  
CC samples, and to prepare mutants or isolate similar sequences from related  
CC species.  
XX  
SQ Sequence 293 BP; 82 A; 60 C; 72 G; 77 T; 2 other;

## Alignment Scores:

Pred. No.:	3,01e-14	Length:	293
Score:	185.00	Matches:	30
Percent Similarity:	86.84%	Conservative:	3
Best Local Similarity:	78.95%	Mismatches:	5
Query Match:	67.27%	Indels:	0
DB:	19	Gaps:	0

US-10-010-731-2 (1-45) x AAV39191 (1-293)

OY 2 ThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHis 21  
Db 176 ACTTGTGAGAAATTTGGCTACATACAGGGACCATGCTTGGTGTGACTTTCAC 235  
OY 22 CysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39  
Db 236 TGCAGAAACCAAGACACTTACTTACGCGNAGGTGAGGAGCAGACTTCGCTGC 289

## RESULT 9

AAQ70126  
ID AAQ70126 standard; cDNA; 141 BP.  
XX  
AC AAQ70126;  
XX  
DT 14-FEB-1995 (first entry)  
XX  
DE Antimicrobial Lc-AFP.  
XX

KM Antimicrobial; Lc-AFP; symbiosis; disease-resistance;  
KM fungus-resistance; Clavibacter xyl subsp. cynodontis; Cxc;  
KM crop improvement; endophyte; ss.

OS Lathyrus cicerca.  
XX  
PN MO9416076-A.  
XX  
PD 21-JUL-1994.  
XX

PF 05-JAN-1994; 94MO-GB00012.  
XX  
PR 08-JAN-1993; 93GB-0000281.  
XX  
PA (ZENE ) ZENECA LTD.  
XX

PI Dubock AC, Powell KA, Rees SB;  
XX  
DR WPI; 1994-249223/30.  
XX  
DR P-PDB; AAR57322.  
XX

PT Antimicrobial protein producing endo-symbiotic microorganisms -  
PT is produced by combining nucleic acids encoding the protein with  
PT an endophyte, useful for protecting plant hosts from esp. fungal  
PT disease  
XX

PS Disclosure; Page 30; 39pp; English.

CC Plant-derived antimicrobial proteins are expressed in endosymbiotic  
CC Clavibacter xyl subsp. cynodontis (Cxc). Plants or seeds treated  
CC with recombinant Cxc are protected against fungal disease. A  
CC suitable antimicrobial protein is Lc-AFP from L. cicerca. A  
CC possible predicted sequence for the Lc-AFP gene is given in AAQ70126.  
XX

SQ Sequence 141 BP; 43 A; 30 C; 32 G; 33 T; 3 other;

## Alignment Scores:

Pred. No.:	1.56e-12	Length:	141
Score:	168.00	Matches:	25
Percent Similarity:	70.21%	Conservative:	8
Best Local Similarity:	53.19%	Mismatches:	12
Query Match:	61.09%	Indels:	2
DB:	15	Gaps:	1

US-10-010-731-2 (1-45) x AAQ70126 (1-141)

OY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18  
Db 1 AAGACTTGGGAGAACCTTCTGTGAACTTTCAGGACCATGCTTCAGATGGAACCTGC 60  
OY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38  
Db 61 AACAGACATTTCAGAGAACAGACGATCTTCTTCTGGAAGATGAGAGATGATTTCCNN 120  
OY 39 CysTrpCysThrLysArgCys 45  
Db 121 TCTGTGTCACACTAGAAACTGC 141

## RESULT 10

AAQ38648  
ID AAQ38648 standard; DNA; 138 BP.  
XX  
AC AAQ38648;  
XX  
DT 07-JUL-1993 (first entry)  
XX  
DE Encodes antifungal protein Lc-AFP1.  
XX  
KM Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Cilloria;  
KM fungicide; bacteriocide; antibiotic; antifungal; gram positive;  
KM plant disease resistance; low toxicity.  
XX  
OS Lathyrus cicerca.



XX	Key	Location/Qualifiers
FH	CDS	1..138
FT		/tag= a
FT		
XX		
PN	MO9305153-A.	
XX		
PD	18-MAR-1993.	
XX		
PF	27-AUG-1992:	92WO-GB01570.
XX		
PR	29-AUG-1991:	91GB-0018523.
PR	13-FEB-1992:	92GB-0003038.
PR	25-JUN-1992:	92SB-0013526.
XX		
PA	(ICIL ) IMPERIAL CHEM IND PLC.	
XX		
PI	Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;	
PI	Vanderleyden J;	
DR	WPI; 1993-100978/12.	
XX		
PT	Biocidal proteins isolated from seeds of plants - e.g. brassica	
PT	or dahlia, useful for increasing plants' resistance to fungal and	
PT	bacterial diseases	
XX		
PS	Disclosure; Fig 31A; 110pp; English.	
XX		
CC	This sequence appears to encode antifungal protein Lc-APPL from	
CC	Lathyrus cicera - see AAR33760. The exact source and isolation of the	
CC	sequence is unclear from the specification.	
SQ	Sequence 138 BP; 43 A; 30 C; 32 G; 33 T; 0 other;	
	Alignment Scores:	
	Pred. No.: 2,28e-11	Length: 138
	Score: 158.50	Matches: 25
	Percent Similarity: 70.21%	Conservative: 8
	Best Local Similarity: 53.19%	Mismatches: 11
	Query Match: 57.64%	Indels: 3
	DB: 14	Gaps: 2
	US-10-010-731-2 (1-45) x AAQ38648 (1-138)	
OY	1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18	
	:::::::::::::::::::::	::::::::::::
Db	1 AACACTGGAGACCTTCGTGCACTTTCAAGGACCATCATTCACAGATGAATACTGC 60	
OY	19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38	
	::: :::::	::::: ::::::::::::::
Dd	61 AACAAACATTGCCAAGAACAAACGACGATCTTCTTGCGAAGATGCAGAGATGATTTC--- 117	
OY	39 CysTrpCysThrLysArgCys 45	
Dd	118 TGCTGGTGCATGAGAATACTGC 138	
	RESULT 11	
ID	AAC34773	
XX	AAC34773 standard; DNA; 487 BP.	
AC	AAC34773:	
DT	17-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 7837.	
XX		
KW	Hybridisation assay; genetic mapping; gene expression control;	
KW	protein identification; signal transduction pathway;	
KW	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
NN	EPI033405-A2.	

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02-JUL-1999; 99US-0142055;
06-JUL-1999; 99US-0142380;
08-JUL-1999; 99US-0142803;
09-JUL-1999; 99US-0142920;
12-JUL-1999; 99US-0142977;
13-JUL-1999; 99US-0143542;
14-JUL-1999; 99US-0143624;
15-JUL-1999; 99US-0144005;
16-JUL-1999; 99US-0144085;
16-JUL-1999; 99US-0144086;
19-JUL-1999; 99US-0144325;
19-JUL-1999; 99US-0144331;
19-JUL-1999; 99US-0144332;
19-JUL-1999; 99US-0144333;
19-JUL-1999; 99US-0144334;
19-JUL-1999; 99US-0144335;
20-JUL-1999; 99US-0144352;
20-JUL-1999; 99US-0144632;
20-JUL-1999; 99US-0144884;
21-JUL-1999; 99US-0144814;
21-JUL-1999; 99US-0145086;
21-JUL-1999; 99US-0145088;
22-JUL-1999; 99US-0145085;
22-JUL-1999; 99US-0145087;
22-JUL-1999; 99US-0145089;
22-JUL-1999; 99US-0145192;
23-JUL-1999; 99US-0145145;
23-JUL-1999; 99US-0145218;
23-JUL-1999; 99US-0145224;
26-JUL-1999; 99US-0145276;
27-JUL-1999; 99US-0145913;
27-JUL-1999; 99US-0145918;
27-JUL-1999; 99US-0145919;
28-JUL-1999; 99US-0145951;
02-AUG-1999; 99US-0146386;
02-AUG-1999; 99US-0146388;
02-AUG-1999; 99US-0146389;
03-AUG-1999; 99US-0147038;
04-AUG-1999; 99US-0147204;
04-AUG-1999; 99US-0147302;
05-AUG-1999; 99US-0147192;
05-AUG-1999; 99US-0147260;
06-AUG-1999; 99US-0147303;
06-AUG-1999; 99US-0147416;
09-AUG-1999; 99US-0147493;
09-AUG-1999; 99US-0147935;
10-AUG-1999; 99US-0148171;
11-AUG-1999; 99US-0148319;
12-AUG-1999; 99US-0148341;
13-AUG-1999; 99US-0148565;
13-AUG-1999; 99US-0148684;
16-AUG-1999; 99US-0149368;
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23-AUG-1999; 99US-0149929;
23-AUG-1999; 99US-0149929;
23-AUG-1999; 99US-0149930;
25-AUG-1999; 99US-0150566;
26-AUG-1999; 99US-0150884;
27-AUG-1999; 99US-0150884;
27-AUG-1999; 99US-0151065;
27-AUG-1999; 99US-0151066;
27-AUG-1999; 99US-0151080;
30-AUG-1999; 99US-0151303;
31-AUG-1999; 99US-0151303;
31-AUG-1999; 99US-0151438;
01-SEP-1999; 99US-0151930;
07-SEP-1999; 99US-0152363;
10-SEP-1999; 99US-0153070;
13-SEP-1999; 99US-0153758;
15-SEP-1999; 99US-0154018;
16-SEP-1999; 99US-0154039;
20-SEP-1999; 99US-0154779;
22-SEP-1999; 99US-0155139;
23-SEP-1999; 99US-0155486;
24-SEP-1999; 99US-0155659;
28-SEP-1999; 99US-0156458;
29-SEP-1999; 99US-0156596;
04-OCT-1999; 99US-0157117;
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07-OCT-1999; 99US-0158029;
08-OCT-1999; 99US-0158232;
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22-OCT-1999; 99US-0160989;
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25-OCT-1999; 99US-0161405;
25-OCT-1999; 99US-0161406;
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26-OCT-1999; 99US-0161360;
26-OCT-1999; 99US-0161361;
28-OCT-1999; 99US-0161920;
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28-OCT-1999; 99US-0161993;
29-OCT-1999; 99US-0162142;

Alignment Scores:
Pred. No.: 0.0246
Score: 91.00
Percent Similarity: 56.25%
Best Local Similarity: 39.58%
Query Match: 33.09%
DB: 21
Gaps: 3

US-10-010-731-2 (1-45) x AAC34773 (1-487)
OY 1 ArgThnCysGluAsnAlaLaspLysTyrArgGlyProCysPheSer-----GlyCys 18
|||||
159 CCGACGCTGACGTCAACAGCCATAGGTTCAAGGCTCATGTGACACACACAACTGT 215
|||||
OY 19 AsprThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAsp---AspPhe 37
|||||
Db 219 GCACAGCGTGTGC---CACACGCAAGCGTTCGGCGGAGCTAAATGCCGCGATTCGCGT 275
|||||
OY 38 ArgCysTTPCysThrLysArgCys 45
|||||
Db 276 CGTGTCTACTCGCACAAGACACTGC 299
|||||

RESULT 12
ID AAA78455
ID AAA78455 standard; DNA; 495 BP.
AC AAA78455;
XX
XX
XX 27-NOV-2000 (first entry)
DE Plant SDF polynucleotide sequence SEQ List 1 NO:77.
DE
DE
KW Plant; corn; Arabidopsis thaliana; sequence-determined DNA fragment;

```

KM SDF; genetic mapping; identification; promoter; structural gene; UTR;  
KW untranslated region; expression control; ds.  
XX Plant.  
OS  
XX  
PN WO200040695-A2.  
XX  
PD 13-JUL-2000.  
XX  
PF 07-JAN-2000; 2000WO-US00466.  
XX  
PR 08-JAN-1999; 99US-0115293.  
XX  
PA (CERE-) CERES INC.  
XX  
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L;  
DR WPI; 2000-465970/40.  
XX  
XX  
PT New corn plant and Arabidopsis thaliana sequence-determined DNA  
PT fragments, useful for expressing gene products and for controlling  
PT expression of a target gene -  
XX  
XX  
PS Claim 1; Page 362; 673pp; English.  
XX  
XX The present invention describes polynucleotides, such as complete cDNA  
CC sequences and/or sequences of genomic DNA encompassing complete genes,  
CC portions of genes, and/or intergenic regions, collectively referred to  
CC as sequence-determined DNA fragments (SDFs), from corn plants and  
CC Arabidopsis thaliana. The SDFs are promoters, structural genes,  
CC untranslated regions (UTRs), or 3' termination sequences. They can be  
CC used for expressing a gene product and controlling expression of a  
CC target gene, either as a promoter, a structural gene, an UTR or as a  
CC 3' termination sequence. They are also useful as tools for genetic  
CC mapping, and identification of a particular individual plant or for  
CC clustering a group of plants with a common trait. AAA78433 to AAA78630  
CC and AAB24605 to AAB25099 represent the specifically claimed  
CC polynucleotide sequences and polypeptides encoded by them given in the  
CC present invention.  
XX  
XX  
SQ Sequence 495 BP; 114 A; 118 C; 99 G; 164 T; 0 other;  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 0.0251 Length: 495  
Score: 91.00 Matches: 19  
Percent Similarity: 56.25% Conservative: 8  
Best Local Similarity: 39.58% Mismatches: 17  
Query Match: 33.09% Indels: 4  
DB: 21 Gaps: 3  
US-10-010-731-2 (1-45) x AAA78455 (1-495)  
OY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18  
DB 163 CGCACGCTGAGTCAAGAGCCATAGCGTCAAGGTCATGTGACACACACAACTGT 222  
OY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAsp---AspPhe 37  
DB 223 GCAACGCTGTGC---CACAAAGAAAGGCTTCGGCGGAGTAATGCCCTGGATTCCGTCGT 279  
OY 38 ArgCysTrpCysThrLysArgCys 45  
DB 280 CGTTGCTACTGCACACAGACACTGC 303  
RESULT 13  
AAA78544  
ID AAA78544 standard; DNA: 552 BP.  
XX  
XX AAA78544:  
XX  
XX 27-NOV-2000 (first entry)  
XX

DE Plant SDF polynucleotide sequence SEQ list 1 NO:387.  
XX  
XX Plant; corn; Arabidopsis thaliana; sequence-determined DNA fragment;  
KW SDF; genetic mapping; identification; promoter; structural gene; UTR;  
KW untranslated region; expression control; ds.  
XX  
XX Plant.  
OS  
XX  
PN WO200040695-A2.  
XX  
PD 13-JUL-2000.  
XX  
PF 07-JAN-2000; 2000WO-US00466.  
XX  
PR 08-JAN-1999; 99US-0115293.  
XX  
PA (CERE-) CERES INC.  
XX  
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;  
PI Zheng L;  
DR WPI; 2000-465970/40.  
XX  
XX  
PT New corn plant and Arabidopsis thaliana sequence-determined DNA  
PT fragments, useful for expressing gene products and for controlling  
PT expression of a target gene -  
XX  
XX  
PS Claim 1; Page 516; 673pp; English.  
XX  
XX The present invention describes polynucleotides, such as complete cDNA  
CC sequences and/or sequences of genomic DNA encompassing complete genes,  
CC portions of genes, and/or intergenic regions, collectively referred to  
CC as sequence-determined DNA fragments (SDFs), from corn plants and  
CC Arabidopsis thaliana. The SDFs are promoters, structural genes,  
CC untranslated regions (UTRs), or 3' termination sequences. They can be  
CC used for expressing a gene product and controlling expression of a  
CC target gene, either as a promoter, a structural gene, an UTR or as a  
CC 3' termination sequence. They are also useful as tools for genetic  
CC mapping, and identification of a particular individual plant or for  
CC clustering a group of plants with a common trait. AAA78433 to AAA78630  
CC and AAB24605 to AAB25099 represent the specifically claimed  
CC polynucleotide sequences and polypeptides encoded by them given in the  
CC present invention.  
XX  
XX  
SQ Sequence 552 BP; 131 A; 126 C; 107 G; 188 T; 0 other;  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 0.0287 Length: 552  
Score: 91.00 Matches: 19  
Percent Similarity: 56.25% Conservative: 8  
Best Local Similarity: 39.58% Mismatches: 17  
Query Match: 33.09% Indels: 4  
DB: 21 Gaps: 3  
US-10-010-731-2 (1-45) x AAA78544 (1-552)  
OY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18  
DB 220 CGCACGCTGAGTCAAGAGCCATAGCGTCAAGGTCATGTGACACACACAACTGT 279  
OY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAsp---AspPhe 37  
DB 280 GCAACGCTGTGC---CACAAAGAAAGGCTTCGGCGGAGTAATGCCCTGGATTCCGTCGT 336  
OY 38 ArgCysTrpCysThrLysArgCys 45  
DB 337 CGTTGCTACTGCACACAGACACTGC 360  
RESULT 14  
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ID AAC44316 standard; DNA: 489 BP.  
XX  
XX AAC44316:  
XX

XX 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 42412.  
DE  
XX  
XX Hybridisation assay: genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
PN  
XX EPI033405-A2.  
PD  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
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PR 06-APR-1999; 99US-0128233.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
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PR 30-APR-1999; 99US-0132040.  
PR 30-APR-1999; 99US-0132407.  
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PR 06-MAY-1999; 99US-0132486.  
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PR 27-MAY-1999; 99US-0136392.  
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PR 17-AUG-1999; 99US-0149175.  
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PR 23-AUG-1999; 99US-0149920.  
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PR 26-AUG-1999; 99US-0150884.

PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
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PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
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PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
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PR 22-OCT-1999; 99US-0160989.  
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PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

## Alignment Scores:

Pred. No.: 0.0581 Length: 489  
Score: 88.00 Matches: 18  
Percent Similarity: 57.45% Conserves: 9  
Best Local Similarity: 38.30% Mismatches: 16  
Query Match: 32.00% Indels: 4  
DB: 21 Gaps: 3

US-10-010-731-2 (1-45) x AAC44316 (1-489)

QY 1 ArgThrcysgluasnluaAlaAsplysTyrArgIlyProcyPheSer-----GlyCys 18  
DB 133 AGAACTGTGTAGTACCAAGTTCACAGGAGCTGTCACACTCACAAGCTGT 192  
QY 19 AspThrIscysThrThrIlysgluAsnAlaValserGlyArgCysArgAspAspPheArg 38  
DB 193 GCCAAAGCTTGCCCTAGC---GAAGGTTTTTCAGCGCGGTGATGT---AGTACGTCTCGCT 246  
QY 39 CysTrpCysThrIlyArgCys 45  
DB 247 TGCTACTGCTCCAAAGCTGCG 267

RESULT 15  
AAC34077  
ID AAC34077 standard; DNA: 526 BP.  
XX  
AC AAC34077;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SRO ID NO: 5364.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
PN EP1033405-A2.  
PD  
XX 06-SEP-2000.  
XX  
PE 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
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PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
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PR 23-JUN-1999; 99US-0140353.  
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PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142053.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
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PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144864.  
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PR 02-AUG-1999; 99US-0146386.  
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PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
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PR 10-AUG-1999; 99US-0148171.  
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PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
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PR 26-AUG-1999; 99US-0150884.  
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PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154038.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
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PR 12-OCT-1999; 99US-0158368.  
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PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
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PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
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PR 26-OCT-1999; 99US-0161359.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
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PR 29-OCT-1999; 99US-0162142.

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Score: 88.00 Matches: 18  
Percent Similarity: 57.45% Conservative: 9  
Best Local Similarity: 38.30% Mismatches: 16  
Query Match: 32.00% Indels: 4  
DB: 21 Gaps: 3

US-10-010-731-2 (1-45) x AAC34077 (1-526)

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Db 133 AGAAGCTTGACAGTACCAAGTACCAAGAGCTTTGTCTCAACATCAGACAGCTGT 192  
QY 19 AspThrIscysThrThrLysGluAsnAlaValSerGIYargCysArgAspPhearg 38



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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 06:15:24 ; Search time 35.4706 Seconds  
(without alignments)  
389.068 Million cell updates/sec

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Perfect score: 275  
Sequence: 1 RICEHLADRYRCPFCFSGCDT.....ENAVSGRCRDRFCRCCKRC 45

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Ygapop 10.0 , Ygapex 0.5  
Fgapop 6.0 , Fgapex 7.0  
Delop 6.0 , Delcxt 7.0

Searched: 441362 seqs, 153338381 residues  
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :  
1: Issued\_Patents\_NA.\*  
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6: /cgn2.6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	275	100.0	250	3	US-08-766-355-13
2	275	100.0	250	4	US-09-003-198A-13
3	275	100.0	250	4	US-09-428-805-13
4	275	100.0	480	4	US-09-003-198A-19
5	275	100.0	507	3	US-08-766-355-10
6	275	100.0	507	3	US-09-003-198A-10
7	275	100.0	507	4	US-09-428-805-10
8	241	87.6	337	4	US-08-766-355-9
9	241	87.6	337	4	US-09-003-198A-9
10	241	87.6	337	4	US-09-428-805-9
11	231.5	84.2	189	4	US-09-003-198A-18
12	231	84.0	200	3	US-08-766-355-5

13	231	84.0	200	4	US-09-003-198A-5	Sequence 5, Appl
14	231	84.0	200	4	US-09-428-805-5	Sequence 5, Appl
15	185	67.3	293	3	US-08-766-355-6	Sequence 6, Appl
16	185	67.3	293	4	US-09-003-198A-6	Sequence 6, Appl
17	185	67.3	293	4	US-09-428-805-6	Sequence 6, Appl
18	168	61.1	141	1	US-08-377-687-35	Sequence 35, Appl
19	168	61.1	141	1	US-08-777-192-35	Sequence 35, Appl
20	168	61.1	141	4	US-08-971-982-35	Sequence 35, Appl
21	81	29.5	47	3	US-08-766-355-12	Sequence 12, Appl
22	81	29.5	47	4	US-09-003-198A-12	Sequence 12, Appl
23	81	29.5	47	4	US-09-428-805-12	Sequence 12, Appl
24	76.5	27.8	363	1	US-08-543-238-6	Sequence 6, Appl
25	76.5	27.8	363	1	US-08-420-526-6	Sequence 6, Appl
26	76.5	27.8	492	1	US-08-543-238-4	Sequence 4, Appl
27	76.5	27.8	492	1	US-08-420-526-4	Sequence 4, Appl
28	72.5	26.4	136	4	US-09-480-251-3	Sequence 3, Appl
29	72.5	26.4	236	4	US-09-480-251-5	Sequence 3, Appl
30	72.5	26.4	488	4	US-09-480-251-1	Sequence 3, Appl
31	72	26.2	147	1	US-08-377-687-36	Sequence 36, Appl
32	72	26.2	147	1	US-08-377-687-36	Sequence 36, Appl
33	72	26.2	147	4	US-08-971-982-36	Sequence 36, Appl
34	70.5	25.6	1981	4	US-08-981-392-26	Sequence 26, Appl
35	70.5	25.6	2663	4	US-09-068-740A-8	Sequence 8, Appl
36	70.5	25.6	8257	4	US-09-484-970B-65	Sequence 65, Appl
37	70	25.5	225	4	US-09-442-631-3	Sequence 3, Appl
38	70	25.5	4403765	4	US-09-103-840A-2	Sequence 2, Appl
39	70	25.5	4411529	4	US-09-103-840A-1	Sequence 1, Appl
40	69	25.1	594	1	US-08-289-458-1	Sequence 1, Appl
41	69	25.1	594	2	US-08-761-549-1	Sequence 1, Appl
42	69	25.1	594	4	US-09-127-646-1	Sequence 1, Appl
43	68.5	24.9	2892	1	US-08-264-534-5	Sequence 5, Appl
44	68.5	24.9	2892	1	US-08-083-590A-1	Sequence 1, Appl
45	68.5	24.9	2892	1	US-08-465-500-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-08-766-355-13  
Sequence 13, Application US/08766355  
Patent No. 612136  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakimi, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,355  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT-063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-766-355-13

Alignment Scores:  
Pred. No.: 2,76e-27 length: 250  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Caps: 0

US-10-010-731-2 (1-45) x US-08-766-355-13 (1-250)

OY 1 ArgThrcysgluasnleualaspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
105 AGAACATGTGAGATTGGCAGATAAATATAGGGACCATGCTTAGTGTGTGACACT 164  
OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArgCysTrp 40  
165 CACTGCACACCAAGAGACGAGTTAGTGGAAGGTGTAGGACGACCTTCCGCTCTGC 224  
DB 41 CysThrLysArgCys 45  
225 TGTACTAAAGATGT 239

RESULT 2  
US-09-003-198A-13  
Sequence 13, Application US/09003198A  
Patent No. 6316407

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakimi, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,198A  
FILING DATE: 07-JAN-1998

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Paterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT:193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-003-198A-13

Alignment Scores:

Pred. No.: 2,76e-27 length: 250  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Caps: 0

US-10-010-731-2 (1-45) x US-09-003-198A-13 (1-250)

OY 1 ArgThrcysgluasnleualaspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
105 AGAACATGTGAGATTGGCAGATAAATATAGGGACCATGCTTAGTGTGTGACACT 164  
OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArgCysTrp 40  
165 CACTGCACACCAAGAGACGAGTTAGTGGAAGGTGTAGGACGACCTTCCGCTCTGC 224  
DB 41 CysThrLysArgCys 45  
225 TGTACTAAAGATGT 239

RESULT 3  
US-09-428-805-13  
Sequence 13, Application US/09428805  
Patent No. 6329504

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakimi, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/428,805  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/766,355  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 474-7577  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-428-805-13

Alignment Scores:  
Pred. No.: 2,76e-27 length: 250  
Score: 275.00 Matches: 45

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-428-805-13 (1-250)

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DB 105 AGACATGTGAGATTGGCAGATAATATAGGGGACCATGCTTAGTGTTGTGACACT 164  
QY 21 HisCysThrThrllysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTyr 40  
|||||  
DB 165 CACTGCACAACCAAGACAGCAGTGAAGGTGTAGGAGCAGACTCCGCTGCTGG 224  
QY 41 CysThrIysArgCys 45  
|||||  
DB 225 TGTACTAAAGATGT 239

## RESULT 4.

US-09-003-198A-19  
; Sequence 19, Application US/09003198A  
; Patent No. 6316407  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakiml, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; NUMBER OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,198A  
; FILING DATE: 07-JAN-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT:193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 787-1400  
; TELEFAX: (713) 787-1440  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 490 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-09-003-198A-19

Alignment Scores:  
Pred. No.: 6.41e-27 Length: 490  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

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QY 41 CysThrIysArgCys 45  
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DB 276 TGTACTAAAGATGT 290

## RESULT 5

US-08-766-355-10  
; Sequence 10, Application US/08766355  
; Patent No. 6121436  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakiml, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; NUMBER OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 77210  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,355  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: MOBT:063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: one-of(17, 424, 485)  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N = A or C or G or T"  
; US-08-766-355-10

Alignment Scores:  
Pred. No.: 6.69e-27 Length: 507  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-010-731-2 (1-45) x US-08-766-355-10 (1-507)

QY 1 ArgThrCysGluAsnLeuAlaAspIysTyrArgGlyProCysPheSerGlyCysAspThr 20  
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Db 173 AGAACAATGCGAATTTGGCAGATTAATATAGGGGACCATGCTTAGTGGTTGACACT 232  
QY 21 HiscysThrThrysgluasnalaValserGlyArgCysArgAspPheArgCysTrp 40  
Db 233 CACTGCACAAACCAAGAACGACGTTAGTGAAGGTGTAGGACGACACTTCCGCTGCTGG 292  
QY 41 CysThrLysArgCys 45  
Db 293 TGTACTAAAGATGT 307

## RESULT 6

US-09-003-198A-10  
; Sequence 10, Application US/09003198A  
; Patent No. 6316407  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakimi, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,198A  
; FILING DATE: 07-Jan-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT:193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 787-1400  
; TELEFAX: (713) 787-1440  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: one-of(17, 424, 485)  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-003-198A-10

Alignment Scores:  
Pred. No.: 6,69e-27 Length: 507  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-010-731-2 (1-45) x US-09-003-198A-10 (1-507)

QY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
Db 173 AGAACAATGCGAATTTGGCAGATTAATATAGGGGACCAATGCTTAGTGGTTGTGACACT 232

QY 21 HiscysThrThrysgluasnalaValserGlyArgCysArgAspPheArgCysTrp 40  
Db 233 CACTGCACAAACCAAGAACGACGTTAGTGAAGGTGTAGGACGACACTTCCGCTGCTGG 292  
QY 41 CysThrLysArgCys 45  
Db 293 TGTACTAAAGATGT 307

## RESULT 7

US-09-428-805-10  
; Sequence 10, Application US/09428805  
; Patent No. 6329504  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakimi, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 77210  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/428,805  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/766,355  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: MOBT:063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: one-of(17, 424, 485)  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-428-805-10

Alignment Scores:  
Pred. No.: 6,69e-27 Length: 507  
Score: 275.00 Matches: 45  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-010-731-2 (1-45) x US-09-428-805-10 (1-507)

QY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
Db 173 AGAACAATGCGAATTTGGCAGATTAATATAGGGGACCAATGCTTAGTGGTTGTGACACT 232

OY 21 H5CysThrThLySGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTrp 40  
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Db 233 CACTGCACAACCAAGACGACGAGTGTAGGAGAGCTTGCCTCCCTCTG 292

OY 41 CysThrLyArgCys 45  
|||||  
Db 293 TGTACTAAAGATGT 307

## RESULT 8

US-08-766-355-9  
; Sequence 9, Application US/08766355  
; Patent No. 6121436  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakimi, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 77210  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,355  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: MOBT:063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: one-of(244, 305)  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-08-766-355-9

## Alignment Scores:

Pred. No.: 8, 87e-23 Length: 327  
Score: 241.00 Matches: 41  
Percent Similarity: 97.62% Conservative: 0  
Best Local Similarity: 97.62% Mismatches: 1  
Query Match: 87.64% Indels: 0  
DB: 3 Gaps: 0

US-10-010-731-2 (1-45) x US-08-766-355-9 (1-327)

OY 4 GluAsnLeuAlaAspLysTrpArgGlyProCysPheSerGlyCysAspThrHisCysThr 23  
|||||  
Db 1 GAGAAATTTGGCGGATAGTAGTACGACCATGCTTTAGTGTGTGACACTCTGCACACA 60  
OY 24 ThrLySGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTrpCysThrLys 43

Db 61 ACCAAGAGAACCCAGTGTAGTGAAGGTAGGAGATGACTTGTGTTAGTACTAA 120  
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OY 44 ArgCys 45  
|||||  
Db 121 AGATGT 126

## RESULT 9

US-09-003-198A-9  
; Sequence 9, Application US/09003198A  
; Patent No. 6316407  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakimi, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,198A  
; FILING DATE: 07-JAN-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT:193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 787-1400  
; TELEFAX: (713) 787-1440  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: one-of(244, 305)  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-003-198A-9

## Alignment Scores:

Pred. No.: 8, 87e-23 Length: 327  
Score: 241.00 Matches: 41  
Percent Similarity: 97.62% Conservative: 0  
Best Local Similarity: 97.62% Mismatches: 1  
Query Match: 87.64% Indels: 0  
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-003-198A-9 (1-327)

OY 4 GluAsnLeuAlaAspLysTrpArgGlyProCysPheSerGlyCysAspThrHisCysThr 23  
|||||  
Db 1 GAGAAATTTGGCGGATAGTAGTACGACCATGCTTTAGTGTGTGACACTCTGCACACA 60  
OY 24 ThrLySGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTrpCysThrLys 43  
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Db 1 ACCAAGAGAACCCAGTGTAGTGAAGGTAGGAGATGACTTGTGTTAGTACTAA 120

OY 44 ArgCys 45  
|||||  
Db 121 AGATGT 126

## RESULT 10

US-09-428-805-9  
; Sequence 9, Application US/09428805  
; Patent No. 6329504  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakim, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 77210  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/428,805  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/766,355  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: MOBT:063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: one-of(244, 305)  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N - A or C or G or T"  
US-09-428-805-9

## Alignment Scores:

Pred. No.: 8 87e-23 length: 327  
Score: 241.00 Matches: 41  
Percent Similarity: 97.628 Conservative: 0  
Best Local Similarity: 97.628 Mismatches: 1  
Query Match: 87.648 Indels: 0  
DB: 4 Gaps: 0

US-10-010-731-2 (1-45) x US-09-428-805-9 (1-327)

OY 4 GluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThrHisCysThr 23  
|||||  
Db 1 GAGAAATTGGCGGATAGATAGGAGCCATGCTTAGTGCTGACACTCAGTCACACA 60  
OY 24 ThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysThrLys 43  
|||||

Db 61 ACCAAGAGAACGCGACTAGTGGAGGTGTAGGATGACTTTGTTAGTGTACTAAA 120  
OY 44 ArgCys 45  
|||||  
Db 121 AGATGT 126

## RESULT 11

US-09-003-198A-18  
; Sequence 18, Application US/09003198A  
; Patent No. 6316407  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip Maganlal  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; APPLICANT: Hakim, Salim  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,198A  
; FILING DATE: 07-JAN-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT:193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 787-1400  
; TELEFAX: (713) 787-1440  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 189 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-09-003-198A-18

## Alignment Scores:

Pred. No.: 7 38e-22 length: 189  
Score: 231.50 Matches: 40  
Percent Similarity: 97.568 Conservative: 0  
Best Local Similarity: 97.568 Mismatches: 0  
Query Match: 84.188 Indels: 1  
DB: 4 Gaps: 1

US-10-010-731-2 (1-45) x US-09-003-198A-18 (1-189)

OY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
|||||  
Db 63 AGAACATGTGAGAAATTGGGAGATTAATATAGGCGACCATGCTTAGTGCTGTGACACT 122  
OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg---Cys 39  
|||||  
Db 123 CACTGCACAACCAAGAGAGACGAGTTAGTGGAGGAGCAGCTTCGCTGCCTGC 182  
OY 40 Trp 40  
|||  
Db 183 TGG 185  
RESULT 12

US-08-766-355-5  
 : Sequence 5, Application US/08766355  
 : Patent No. 6121436  
 : GENERAL INFORMATION:  
 : APPLICANT: Liang, Jihong  
 : APPLICANT: Shah, Dilip Meganalal  
 : APPLICANT: Wu, Yonnie S.  
 : APPLICANT: Rosenberger, Cindy A.  
 : APPLICANT: Hakimi, Salim  
 : TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
 : Controlling Plant Pathogenic Fungi  
 : NUMBER OF SEQUENCES: 14  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Arnold, White & Durkee  
 : STREET: P.O. Box 77210  
 : CITY: Houston  
 : STATE: Texas  
 : COUNTRY: United States of America  
 : ZIP: 77210  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC compatible  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/766,355  
 : FILING DATE: Concurrently Herewith  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Mitchell, Barbara S.  
 : REGISTRATION NUMBER: 33,928  
 : REFERENCE/DOCKET NUMBER: MOBT:063  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (512) 418-3000  
 : TELEFAX: (512) 474-7577  
 : INFORMATION FOR SEQ ID NO: 5:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 200 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : FEATURE:  
 : NAME/KEY: modified\_base  
 : LOCATION: 17  
 : OTHER INFORMATION: /mod\_base= OTHER  
 : OTHER INFORMATION: /note= "N = A or C or G or T"  
 : US-08-766-355-5  
 : Alignment Scores:  
 : Pred. No.: 9.19e-22 Length: 200  
 : Score: 231.00 Matches: 39  
 : Percent Similarity: 100.00% Conservative: 0  
 : Best Local Similarity: 100.00% Mismatches: 0  
 : Query Match: 84.00% Indels: 0  
 : DB: 3 Gaps: 0  
 : US-10-010-731-2 (1-45) x US-08-766-355-5 (1-200)  
 : OY 1 ArgThrcysgluasleuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
 : |||||||  
 : DB 80 AGACATGTGAGATTTGGCAGATAAATATAGGGGACCATCTTAGTGTTGACACT 139  
 : OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39  
 : |||||||  
 : DB 140 CACTGCACAAACCAAGAGACGAGTTAGTGGAAGGTGTAGGAGCAGACTTCCGCTGC 196  
 : RESULT 13  
 : US-09-003-198A-5  
 : Sequence 5, Application US/09003198A  
 : Patent No. 6316407  
 : GENERAL INFORMATION:  
 : APPLICANT: Liang, Jihong  
 : APPLICANT: Shah, Dilip Meganalal

APPLICANT: Wu, Yonnie S.  
 APPLICANT: Rosenberger, Cindy A.  
 APPLICANT: Hakimi, Salim  
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
 Controlling Plant Pathogenic Fungi  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/003,198A  
 FILING DATE: 07-JAN-1998  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paterson, Melinda L.  
 REGISTRATION NUMBER: 33,062  
 REFERENCE/DOCKET NUMBER: MOBT:193  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (713) 787-1400  
 TELEFAX: (713) 787-1440  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 200 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: 17  
 OTHER INFORMATION: /mod\_base= OTHER  
 OTHER INFORMATION: /note= "N = A or C or G or T"  
 : US-09-003-198A-5  
 : Alignment Scores:  
 : Pred. No.: 9.19e-22 Length: 200  
 : Score: 231.00 Matches: 39  
 : Percent Similarity: 100.00% Conservative: 0  
 : Best Local Similarity: 100.00% Mismatches: 0  
 : Query Match: 84.00% Indels: 0  
 : DB: 4 Gaps: 0  
 : US-10-010-731-2 (1-45) x US-09-003-198A-5 (1-200)  
 : OY 1 ArgThrcysgluasleuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
 : |||||||  
 : DB 80 AGACATGTGAGATTTGGCAGATAAATATAGGGGACCATCTTAGTGTTGACACT 139  
 : OY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39  
 : |||||||  
 : DB 140 CACTGCACAAACCAAGAGACGAGTTAGTGGAAGGTGTAGGAGCAGACTTCCGCTGC 196  
 : RESULT 14  
 : US-09-428-805-5  
 : Sequence 5, Application US/09428805  
 : Patent No. 6329504  
 : GENERAL INFORMATION:  
 : APPLICANT: Liang, Jihong  
 : APPLICANT: Shah, Dilip Meganalal  
 : APPLICANT: Wu, Yonnie S.  
 : APPLICANT: Rosenberger, Cindy A.  
 : APPLICANT: Hakimi, Salim  
 : TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
 : Controlling Plant Pathogenic Fungi  
 : NUMBER OF SEQUENCES: 14

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 17
OTHER INFORMATION: /mod_base- OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-428-805-5

Alignment Scores:
Pred. No.: 9,19e-22 Length: 200
Score: 231.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.00% Indels: 0
DB: 4 Gaps: 0

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QY 21 HisGysThrThrlysgluasnlalavalSerGlyArgCysArgaspPheargCys 39
Db 140 CACTGCACACCAAGAACGACGATTAGTGAGAGGTGTAGGAGCAGACTTCCGCTGC 196

RESULT 15
US-08-766-355-6
Sequence 6, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
CONTROLLING Plant: Pathogenic Fungi
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
```

```

CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base- OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-6

Alignment Scores:
Pred. No.: 1,18e-15 Length: 293
Score: 185.00 Matches: 30
Percent Similarity: 86.84% Conservative: 3
Best Local Similarity: 78.95% Mismatches: 5
Query Match: 67.27% Indels: 0
DB: 3 Gaps: 0

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QY 22 CysThrThrlysgluasnlalavalSerGlyArgCysArgaspPheargCys 39
Db 236 TGCMAAACCAAGACACTTACTTAGCGNAGGTGACGAGCAGCACTTCCCTGC 289

Search completed: June 21, 2003, 07:53:49
Job time : 40.4706 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 07:19:24 ; Search time 110.118 Seconds  
(without alignments)  
599.670 Million cell updates/sec

Title: US-10-010-731-2  
Perfect score: 275  
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Ygapop 10.0, Ygapext 0.5  
Delop 6.0, Delext 7.0

Searched: 1042519 segs, 733713590 residues  
Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database: 1: Published.Applications.NA:

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4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the total being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	275	100.0	480	9	US-10-010-731-19
3	275	100.0	507	9	US-10-010-731-10
4	241	87.6	327	9	US-10-010-731-9

5	231.5	84.2	189	9	US-10-010-731-18	Sequence 18, App1
6	231	84.0	200	9	US-10-010-731-5	Sequence 5, App1
7	206	74.9	461	9	US-10-178-213-451	Sequence 451, App
8	206	74.9	494	9	US-09-805-694B-5	Sequence 5, App1
9	205.5	74.7	420	9	US-10-178-213-436	Sequence 436, App
10	203	73.8	563	9	US-10-178-213-439	Sequence 439, App
11	185	67.3	293	9	US-10-010-731-6	Sequence 6, App1
12	168	61.1	141	10	US-09-759-584-35	Sequence 35, App1
13	157.5	57.3	464	9	US-10-178-213-379	Sequence 379, App
14	104	37.8	635	9	US-10-178-213-37	Sequence 37, App
15	103	37.5	222	10	US-09-878-574-10791	Sequence 10791, A
16	103	37.5	277	10	US-09-878-574-11794	Sequence 11794, A
17	103	37.5	361	10	US-09-878-574-1139	Sequence 1139, Ap
18	103	37.5	466	9	US-10-178-213-385	Sequence 385, App
19	102	37.1	504	9	US-10-178-213-409	Sequence 409, App
20	100.5	36.5	573	9	US-10-178-213-403	Sequence 403, App
21	100	36.4	275	10	US-09-878-574-14296	Sequence 14296, A
22	98	35.6	425	9	US-10-178-213-325	Sequence 325, App
23	98	35.6	587	9	US-10-178-213-331	Sequence 331, App
24	97	35.3	469	9	US-10-178-213-433	Sequence 433, App
25	97	35.3	523	9	US-10-178-213-412	Sequence 412, App
26	96	34.9	553	9	US-10-178-213-340	Sequence 340, App
27	96	34.9	445	9	US-10-178-213-343	Sequence 343, App
28	96	34.9	459	9	US-10-178-213-334	Sequence 334, App
29	92.5	33.6	471	9	US-10-178-213-100	Sequence 100, App
30	91	33.1	399	9	US-10-178-213-337	Sequence 337, App
31	91	33.1	448	9	US-10-178-213-406	Sequence 406, App
32	91	33.1	478	9	US-10-178-213-307	Sequence 307, App
33	90	32.7	557	9	US-10-178-213-28	Sequence 28, App1
34	89.5	32.5	264	10	US-09-878-574-13620	Sequence 13620, A
35	89	32.4	447	9	US-10-178-213-445	Sequence 445, App
36	89	32.4	473	9	US-10-178-213-448	Sequence 448, App
37	88	32.0	465	9	US-10-178-213-34	Sequence 34, App1
38	88	32.0	507	9	US-10-178-213-70	Sequence 70, App1
39	88	32.0	534	9	US-10-178-213-103	Sequence 103, App
40	87.5	31.8	441	9	US-10-178-213-106	Sequence 106, App
41	87	31.6	234	9	US-09-938-842A-617	Sequence 617, App
42	87	31.6	468	9	US-10-178-213-97	Sequence 97, App1
43	87	31.6	524	9	US-10-178-213-442	Sequence 442, App
44	86	31.3	363	9	US-10-178-213-124	Sequence 124, App
45	86	31.3	367	9	US-10-178-213-121	Sequence 121, App

#### ALIGNMENTS

RESULT 1  
US-10-010-731-13  
; Sequence 13, Application US/10010731  
; Publication No. US20030041347A1  
GENERAL INFORMATION:

APPLICANT: Liang, Jihong  
Shah, Dilip Maganlal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433

CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010.731

FILING DATE: 13-NO. US20030041347A1-2001

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/003,198
  FILING DATE: 07-JAN-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: Paterson, Melinda L.
    REGISTRATION NUMBER: 33,062
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (713) 787-1400
    TELEFAX: (713) 787-1440
  INFORMATION FOR SEQ ID NO: 13:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 250 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

Alignment Scores:
Pred. No.: 6,25e-30      Length: 250
Score: 275.00           Matches: 45
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                   Gaps: 0

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QY 21 HisCysThrHrlysgIuAsnAlaValSerGlyArgCysArgAspPheArgCysTrp 40
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DB 165 CACTGCACACCAAGAAGACGCAGTTAGTGAAGGTGTAGGAGCAGACTTCCTCGCTGG 224
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QY 41 CysThrLysArgCys 45
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DB 225 TGTACTAAAGATGT 239

RESULT 2
US-10-010-731-19
  Sequence 19, Application US/10010731
  Publication No. US20030041347A1
  GENERAL INFORMATION:
    APPLICANT: Liang, Jihong
    Wu, Yonnie S.
    Rosenberger, Cindy A.
    Hakimi, Salim
  TITLE OF INVENTION: Antifungal Polypeptide and Methods for
    Controlling Plant Pathogenic Fungi
  NUMBER OF SEQUENCES: 19
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: Texas
    COUNTRY: USA
    ZIP: 77210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/010,731
    FILING DATE: 13-NO. US20030041347A1-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/003,198
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FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
  NAME: Paterson, Melinda L.
  REGISTRATION NUMBER: 33,062
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (713) 787-1400
    TELEFAX: (713) 787-1440
  INFORMATION FOR SEQ ID NO: 19:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 490 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

Alignment Scores:
Pred. No.: 1,46e-29      Length: 490
Score: 275.00           Matches: 45
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                   Gaps: 0

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QY 21 HisCysThrHrlysgIuAsnAlaValSerGlyArgCysArgAspPheArgCysTrp 40
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DB 216 CACTGCACACCAAGAAGACGCAGTTAGTGAAGGTGTAGGAGCAGACTTCCTCGCTGG 275
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QY 41 CysThrLysArgCys 45
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DB 276 TGTACTAAAGATGT 290

RESULT 3
US-10-010-731-10
  Sequence 10, Application US/10010731
  Publication No. US20030041347A1
  GENERAL INFORMATION:
    APPLICANT: Liang, Jihong
    Wu, Yonnie S.
    Rosenberger, Cindy A.
    Hakimi, Salim
  TITLE OF INVENTION: Antifungal Polypeptide and Methods for
    Controlling Plant Pathogenic Fungi
  NUMBER OF SEQUENCES: 19
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: Texas
    COUNTRY: USA
    ZIP: 77210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/010,731
    FILING DATE: 13-NO. US20030041347A1-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/003,198
    FILING DATE: 07-JAN-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: Paterson, Melinda L.
```

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:      REGISTRATION NUMBER: 33,062
:      REFERENCE/DOCKET NUMBER: MOBI:193
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (713) 787-1400
:      TELEFAX: (713) 787-1440
:      INFORMATION FOR SEQ ID NO: 10:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 507 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: linear
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:      FEATURE:
:      NAME/KEY: modified_base
:      LOCATION: one-of(17, 424, 485)
:      OTHER INFORMATION: /mod_base= OTHER
:      /note= "N = A or C or G or T"
:      SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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:      Best Local Similarity:      100.00%      Mismatches:      0
:      Query Match:      100.00%      Indels:      0
:      DB:      9      Gaps:      0
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:      DB      173      AGAACATTTGTGACAATTTGGCAGATAAATVATAGGGGACCATGCTTGTAGTGTGTGACACT 232
:      QY      21      HISCSTRTTHLYGLUASNAIAlaValserGLYArgCYsArGspAspPheArgCYSTp 40
:      DB      233      CACTGCACACCAAGAGACAGCCAGTTAGTGCAGAGCTGAGGGACGACACTCCGCTGCTGG 232
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:      QY      41      CysthrLYsArgCYs 45
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:      RESULT 4
:      ; Sequence 9, Application US/10010731
:      ; Publication No. US20030041347A1
:      ; GENERAL INFORMATION:
:      ; APPLICANT: Liang, Jihong
:      ;      Shah, Dilip Maganlal
:      ;      Wu, Yonnie S.
:      ;      Rosenberger, Cindy A.
:      ;      Hakim, Salim
:      ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
:      ;      Controlling Plant Pathogenic Fungi
:      ; NUMBER OF SEQUENCES: 19
:      ; CORRESPONDENCE ADDRESS:
:      ;      ADDRESSEE: Arnold White & Durkee
:      ;      STREET: P.O. Box 4433
:      ;      CITY: Houston
:      ;      STATE: Texas
:      ;      COUNTRY: USA
:      ;      ZIP: 77210
:      ; COMPUTER READABLE FORM:
:      ;      MEDIUM TYPE: Floppy disk
:      ;      COMPUTER: IBM PC compatible
:      ;      OPERATING SYSTEM: PC-DOS/MS-DOS
:      ;      SOFTWARE: PatentIn Release #1.0, Version #1.30
:      ; CURRENT APPLICATION DATA:
:      ;      APPLICATION NUMBER: US/10/010,731
:      ;      FILING DATE: 13-NO. US20030041347A1-2001
:      ;      CLASSIFICATION: <Unknown>
:      ; PRIOR APPLICATION DATA:
:      ;      APPLICATION NUMBER: 09/003,198
:      ;      FILING DATE: 07-JAN-1998
:

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ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base= OTHER
/note="N = A or C or G or T"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-010-731-9

Alignment Scores:
Pred. No.:      4.95e+25           Length:          327
Score:         241.00             Matches:          41
Percent Similarity:   97.62%       Conservative:     0
Best Local Similarity: 97.62%       Mismatches:      1
Query Match:        87.64%         Indels:          0
DB:                9              Gaps:            0

US-10-010-731-2 (1-45) x US-10-010-731-9 (1-327)
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Db    1 GAGAAATTTGGCGGATAAGTATAGGGGACCATGCTTAGTGTTGTGCACACTCACTGCACA 60
      | |||||

QY    24 ThrLysGUAsrAlaValserGLyArGcSArGaSPasPhearGcyStrPCystrIrrls 43
      | |||||
Db    61 ACCAAAGAGAACGCCAGTTAGTGAAGGTATAGGATGACTTCGTTGTTAGTACTAAA 120
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QY    44 ArGcys 45
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Db    121 AGATGT 126

RESULT 5
US-10-010-731-18
; Sequence 18, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30.
APPLICATION NUMBER: US/10/010-731
FLING DATE: 13-No. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 09/003,198  
FILING DATE: 07-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Paterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 189 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-010-731-18

Alignment Scores:  
Pred. No.: 5,27e-24 Length: 189  
Score: 231.50 Matches: 40  
Percent Similarity: 97.56% Conservative: 0  
Best Local Similarity: 97.56% Mismatches: 0  
Query Match: 84.18% Indels: 1  
DB: 9 Gaps: 1

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DB 63 AGAACATGTAGATTTGGCAGATAATATAGGGGACCATGCTTACTGTGGACACT 122  
|||||

QY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArg---Cys 39  
|||||  
DB 123 CACTGCACCAACCAAGAGACGAGTGTAGTGAAGGTGTAGGACGACGACTTCCGCTGCTGC 182  
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QY 40 Trp 40  
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DB 183 TGG 185

RESULT 6  
US-10-010-731-5  
Sequence 5, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip Maganlal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim  
TITLE OF INVENTION: Antifungal polypeptide and Methods for  
Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,731  
FILING DATE: 13-No. US20030041347A1-2001  
CLASSIFICATION DATA:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/003,198  
FILING DATE: 07-JAN-1998  
ATTORNEY/AGENT INFORMATION:

NAME: Paterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT.193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 200 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 17  
OTHER INFORMATION: /mod\_base= OTHER  
/note="N" = A or C or G or T"  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-010-731-5

Alignment Scores:  
Pred. No.: 6,65e-24 Length: 200  
Score: 231.00 Matches: 39  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 84.00% Indels: 0  
DB: 9 Gaps: 0

US-10-010-731-2 (1-45) x US-10-010-731-5 (1-200)

QY 1 ArgThCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
|||||  
DB 80 AGAACATGTAGATTTGGCAGATAATATAGGGGACCATGCTTACTGTGGACACT 139  
|||||

QY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspPheArgCys 39  
|||||  
DB 140 CACTGCACCAACCAAGAGACGAGTGTAGTGAAGGTGTAGGACGACGACTTCCGCTGC 196  
|||||

RESULT 7  
US-10-178-213-451  
Sequence 451, Application US/10178213  
Publication No. US20030041348A1  
GENERAL INFORMATION:  
APPLICANT: Simmons, Carl R.  
APPLICANT: Navarro Acevedo, Pedro A.  
APPLICANT: Harvell, Leslie  
APPLICANT: Cahoon, Rebecca  
APPLICANT: McCutchen, Billy Fred  
APPLICANT: Lu, Albert  
APPLICANT: Herrmann, Rafael  
TITLE OF INVENTION: Defensein Polynucleotides and Methods of  
FILE REFERENCE: 35718/246703  
CURRENT APPLICATION NUMBER: US/10/178,213  
CURRENT FILING DATE: 2002-06-21  
PRIORITY APPLICATION NUMBER: 60/300,152  
PRIORITY FILING DATE: 2001-06-22  
PRIORITY APPLICATION NUMBER: 60/300,241  
PRIORITY FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 451  
LENGTH: 461  
TYPE: DNA  
ORGANISM: Arachis hypogaea  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (44)...(271)  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (128)...(268)  
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451

Alignment Scores:
Pred. No.: 5.94e-20 Length: 461
Score: 206.00 Matches: 33
Percent Similarity: 80.43% Conservative: 4
Best Local Similarity: 71.74% Mismatches: 7
Query Match: 74.91% Indels: 2
DB: 9 Gaps: 1

US-10-010-731-2 (1-45) x US-10-178-213-451 (1-461)

QY 2 ThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCysAsp 19
   |||||||
Db 131 AGGTGTGAGAACCTGGCGATCTACAGGGACGACATGCTTCCACCGCAAGCTGCGAC 190
   |||||||

QY 20 ThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCys 39
   |||||||
Db 191 GACCACTGCAAGACAGAGAGACACCTGCTCAGGGCGCGCTGCCGCGACATTTCCGCTGT 250
   |||||||

QY 40 TrpCysThrLysArgCys 45
   |||||||
Db 251 TGTGTGACCAACAACACTGT 268

RESULT 8
US-09-805-694B-5
; Sequence 5, Application US/09805694B
; Publication No. US20030041350A1
; GENERAL INFORMATION:
; APPLICANT: Kinney, Anthony
; TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
; FILE REFERENCE: B1432 US NA
; CURRENT APPLICATION NUMBER: US/09/805,694B
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,823
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (9)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (388)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (392)..(393)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (460)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (463)
; OTHER INFORMATION: n = A, C, G, or T
; NAME/KEY: unsure
; LOCATION: (468)
; OTHER INFORMATION: n = A, C, G, or T
US-09-805-694B-5

Alignment Scores:
Pred. No.: 6.48e-20 Length: 494
Score: 206.00 Matches: 33
Percent Similarity: 78.72% Conservative: 4
Best Local Similarity: 70.21% Mismatches: 8
Query Match: 74.91% Indels: 2
DB: 9 Gaps: 1
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```
US-10-010-731-2 (1-45) x US-09-805-694B-5 (1-494)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18
   ::|||
Db 130 AACACTTGCAGAACCTGGCGATCTACAGGGGTCACATGCTTCCACCGCAAGCTGCG 189
   ::|||

QY 19 AspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArg 38
   ||| |||||
Db 190 GATGATCAGTCGCAAGACAAAGAGCACTTCTCAGAGCGAGATGACAGCGACATTTTCGC 249
   ||| |||||

QY 39 CysTrpCysThrLysArgCys 45
   |||||||
Db 250 TGTGTGACCAACAACACTGT 270

RESULT 9
US-10-178-213-436
; Sequence 436, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Cyamopsis tetragonoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(264)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (118)..(261)
US-10-178-213-436

Alignment Scores:
Pred. No.: 6.2e-20 Length: 420
Score: 205.50 Matches: 33
Percent Similarity: 79.17% Conservative: 5
Best Local Similarity: 68.75% Mismatches: 7
Query Match: 74.73% Indels: 3
DB: 9 Gaps: 1

US-10-010-731-2 (1-45) x US-10-178-213-436 (1-420)

QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGly-----GlyCys 17
   ::|||
Db 118 AACAGCATGTGAGATCTTGCAGATACATTCAGGGGTCATGCTTCCCTGGAACCGCAGC 177
   ::|||

QY 18 CysAspThrHisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPhe 37
   |||::|
Db 178 TGCAGAGATCAGTCGCAAGACAAAGAGCACTTCTCAGAGCGAGATGACAGCGATTTT 237
   |||::|

QY 38 ArgCysTrpCysThrLysArgCys 45
   |||||||
Db 238 CGCTGCTGTGTCACCAAAACTGT 261
   |||||||
```

```

1 STREET: P. O. Box 4433
2 CITY: Houston
3 STATE: Texas
4 COUNTRY: USA
5 ZIP: 77210
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent in Release #1.0, Version #1.30
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/10/010,731
14 FILING DATE: 13-Nov-20030041347A1-2001
15 CLASSIFICATION: <Unknown>
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 09/003,198
19 FILING DATE: 07-JAN-1998
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Paterson, Melinda L.
22 REGISTRATION NUMBER: 33,062
23 REFERENCE/DOCKET NUMBER: MOBT:193
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (713) 787-1400
26 TELEFAX: (713) 787-1440
27
28 INFORMATION FOR SEQ ID NO: 6:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 293 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: double
33 TOPOLOGY: linear
34
35 FEATURE:
36 NAME/KEY: modified_base
37 LOCATION: one-of(17, 265)
38 OTHER INFORMATION: /mod_base= OTHER
39 /note= "N = A or C or G or T"
40
41 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
42
43 US-10-010-731-6
44
45 Alignment Scores:
46 Pred. No.:
47 Score: 2.89e-17 Length: 293
48 Percent Similarity: 185.00 Matches: 30
49 Best Local Similarity: 86.848 Conservative: 3
50 Query Match: 78.958 Mismatches: 5
51 DB: 67.278 Indels: 0
52 Gaps: 0
53
54 US-10-010-731-2 (1-45) x US-10-010-731-6 (1-293)
55
56 QY 2 ThcCysgluAsnLeuAlaAspIysTyrArgGlyProCysPheSerGlyCysAspThrHis 21
57 |||||
58 DB 176 ACTTGTGACGATTTGGCTTAACACAAACAGGCGACCATCTTCGGTGGTGGACATTTCAC 235
59 |||||
60 QY 22 CysThrThrlGlyGluAsnAlaValAsrGlyArgCysArgAspAspPheArgCys 39
61 |||||
62 DB 236 TGCAAACCAAGAACACTTACTTAGCGGAGGTGCAGGAGCACTTCGCTGC 289
63 |||||
64
65 RESULT 12
66 US-09-759-584-35
67 Sequence 35, Application US/09759584
68 Patent No. US20010014732A1
69
70 GENERAL INFORMATION:
71 APPLICANT: BROEKAERT, WILLEM F.
72 APPLICANT: CAMMUE, BRUNO P.A.
73 APPLICANT: OSHORN, RUPERT W.
74 APPLICANT: REES, SARAH B.
75 APPLICANT: TERRAS, FRANKY R.G.
76 APPLICANT: VANDERLEYDEN, JOZEF
77 TITLE OF INVENTION: BIOCIDAL PROTEINS
78 NUMBER OF SEQUENCES: 59
79 CORRESPONDENCE ADDRESS:
80 ADDRESSEE: CUSHMAN DARBY & CUSHMAN
81 STREET: 1100 NEW YORK AVENUE, N.W.
82 CITY: WASHINGTON

```







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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 06:14:34 ; Search time 1048.24 Seconds

(without alignments)  
695.261 Million cell updates/sec

Title: US-10-010-731-2

Perfect score: 275

Sequence: 1 RTCENLADKXRGPCFSGCDT.....ENAVSGRCRDPFRCTKRC 45

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=framet\_p2n.model -DEV=xlh

-O/cgnt2\_1/uspro.spool/us10010731/runat\_17062003\_095705\_28177/app\_query.fasta.1.398

-DB-EST -OPMT=fastcap -SUFFIX=ist -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=Blomsum62 -TRANS=human40.cdi -LIST=45

-DOCLGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-USRR=us10010731.ecgn.1.1.2463 @runat.17062003.095705.28171 -NCPU=3

-NO\_MMAP -LARGEQUERY -NEG\_SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estlin:\*

4: em\_estlm:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estlom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vtc:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	97.1	446	9	AJ498901
2	197	71.6	487	13	B1321179
3	172	62.5	426	12	BG838678
4	171	62.2	517	9	AJ308155
5	154.5	56.2	574	14	BO151477
6	141.5	51.5	503	12	BF633403
7	136	49.5	366	13	B1321308
8	116	42.2	438	13	B1642728
9	108	39.3	442	13	BM110496
10	104	37.8	187	12	BF598147
11	104	37.8	292	10	AM203222
12	104	37.8	485	14	BO249330
13	104	37.8	485	13	B1299919
14	104	37.8	492	13	BJ298033
15	104	37.8	502	12	BG838277
16	104	37.8	506	12	BG838599
17	104	37.8	522	13	BJ296553
18	104	37.8	522	12	BG838299
19	104	37.8	526	13	BJ293856
20	104	37.8	566	13	BJ290214
21	103	37.5	212	10	BE611505
22	103	37.5	238	12	BG238242
23	103	37.5	259	12	BG405833
24	103	37.5	295	13	B1469191
25	103	37.5	300	13	B1972271
26	103	37.5	314	10	BE611109
27	103	37.5	323	9	A1495809
28	103	37.5	336	13	B1787994
29	103	37.5	356	12	BE805922
30	103	37.5	356	13	BE805922
31	103	37.5	359	9	A1441508
32	103	37.5	364	10	AM396579
33	103	37.5	364	13	B1788286
34	103	37.5	376	10	AM734140
35	103	37.5	378	10	AM733894
36	103	37.5	390	13	B1972041
37	103	37.5	393	13	BM143218
38	103	37.5	400	9	A1938187
39	103	37.5	403	12	BG041846
40	103	37.5	407	14	BQ081406
41	103	37.5	409	13	B1972131
42	103	37.5	420	13	B1971605
43	103	37.5	420	14	BM954394
44	103	37.5	420	14	BQ080027
45	103	37.5	420	14	BQ080612

## ALIGNMENTS

RESULT 1  
AJ498901  
LOCUS  
DEFINITION AJ498901 MTP0SE Medicago truncatula cDNA clone mt--acc955209h10,  
ACCESSION AJ498901  
VERSION AJ498901.1 GI:22089344  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
barrel medic.  
Medicago truncatula  
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
Spermatophyta: Magnoliophyta: endicotsyledons: core endicots:  
Rosidae: eurosids II: Fabales: Fabaceae: Papilionoideae: Trifoliaceae:  
Medicago.  
REFERENCE  
1 (bases 1 to 446)

**AUTHORS** Firtinhaber, C., Bartelsmeier, V., Meyer, F., Bartels, D., Bekel, T., Linke, B., Puhler, A., and Kuester, H.  
**TITLE** Determination of transcript sequences from developing pods including seeds of Medicago truncatula genotype A17  
**JOURNAL** unpublished (2002)  
**COMMENT** Contact: Kuester H  
 Lehrstuhl fuer Genetik  
 Universitaet Bielefeld  
 Postfach 100131, D-33501 Bielefeld, Germany.  
**FEATURES** Location/Qualifiers  
 source 1. 446  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3860"  
 /clone="mt-acc95209h10"  
 /clone\_1lb="MP0SE"  
 /tissue\_type="pods including seeds"  
 /dev\_stage="different stages of development"  
 /note="vector: pGEM-T; Site\_1: PstI; Site\_2: SphI; genotype A17; cDNA was prepared from polyA+ enriched RNA from developing pods including seeds harvested at different stages of development. The cDNA was directionally ligated by Medigenomix into the pGEM-T vector from Promega using GCATCGCGCCGCGCCGCGCAGC and CTCGAGCCCATATGCGCCGCGG adapters. Plasmids containing cDNA inserts were propagated in E. coli DH10B cells."  
**BASE COUNT** 147 a 84 c 83 g 132 t  
**ORIGIN**  
 Alignment Scores:  
 Pred. NO.: 3.5e-24 Length: 446  
 Score: 267.00 Matches: 43  
 Percent Similarity: 97.78% Conservative: 1  
 Best Local Similarity: 95.56% Mismatches: 1  
 Query Match: 97.09% Indels: 0  
 DB: 9 Gaps: 0  
 US-10-010-731-2 (1-45) x AJ998901 (1-446)  
 QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSerGlyCysAspThr 20  
 Db 142 AAGACTTGAGTGGATTTGGCTGATTAATACAGGGACCATCTTAGTGTTGATACT 201  
 QY 21 HisCysThrThrLysGluAsnAlaValSerGlyArgCysArgAspAspPheArgCysTrp 40  
 Db 202 CACTGCACCTACCAAGAGAAATGACGCGGAGTGACGATGACTTCGTTGTTGG 261  
 QY 41 CysThrLysArgCys 45  
 Db 262 TGTACTATAAACTGT 276

**RESULT 2** BI321179 487 bp mRNA linear EST 29-NOV-2001  
**LOCUS** saf48610.y3 Gm-cl077 glycine max cDNA clone GENOME SYSTEMS CLONE  
**DEFINITION** ID: Gm-cl077-1723 5', similar to SW:10KD\_VIGUN P18646 10 KD PROTEIN  
**ACCESSION** BI321179.1 GI:15000365  
**VERSION** BI321179.1  
**KEYWORDS** EST.  
**SOURCE** soybean.  
**ORGANISM** Glycine max  
 Euarvota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
**REFERENCE** 1 (bases 1 to 487)  
**AUTHORS** Shoemaker, R., Keim, P., Vockin, L., Erpeiding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
**TITLE** Public soybean EST Project

**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Putative full length read  
 vector to vector length is 715  
 Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801  
 for further information call: (800)-533-4363 or contact via email: csh@esgen.com  
 Seq primer: -48RP from Gibco  
 High quality sequence stop: 432.  
**FEATURES** Location/Qualifiers  
 source 1. 487  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl077-1723"  
 /clone\_1lb="Gm-cl077"  
 /tissue\_type="18 day old 'Williams' seedlings"  
 /dev\_stage="18 day old 'Williams' seedlings"  
 /lab\_host="DH10B"  
 /note="vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The mRNA was isolated from cotyledons of 18-day-old 'Williams' seedlings which were greenhouse grown in potting soil. The cotyledons were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer (GAGACAGACAGACAGACAGACTACTCTCGAC(7189) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (400U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."  
**BASE COUNT** 152 a 96 c 102 g 137 t  
**ORIGIN**  
 Alignment Scores:  
 Pred. NO.: 3.13e-15 Length: 487  
 Score: 197.00 Matches: 32  
 Percent Similarity: 76.60% Conservative: 4  
 Best Local Similarity: 68.09% Mismatches: 9  
 Query Match: 71.64% Indels: 2  
 DB: 13 Gaps: 1  
 US-10-010-731-2 (1-45) x BI321179 (1-487)  
 QY 1 ArgThrCysGluAsnLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18  
 Db 152 AAGACTTGCGAGAACCGCGCGATACATACAGGGGCTCCATCGCTACACCTGCGACGCTGC 211  
 QY 19 AspThrCysThrThrLysGluAsnAlaValSerLysArgCysArgAspAspPheArg 38

Db 212 GATGATTTCGACAGACAAGACACTTGTCTCAGAGGAGATGACAGGACGATTTTCGC 271  
QY 39 CystPCysThrLysArgCys 45  
|||||  
Db 272 TGTGTGTCACCAAAACTGT 292

RESULT 3  
Bg838678/c 426 bp mRNA linear EST 25-MAY-2001  
LOCUS Bg838678/c  
DEFINITION glycine clandestina cDNA clone Gc01\_03f01, mRNA sequence.  
ACCESSION Bg838678  
VERSION Bg838678.1 GI:14204985  
KEYWORDS EST.  
SOURCE glycine clandestina.  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
REFERENCE 1 (bases 1 to 426)  
Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.  
Expressed Sequence Tags from Cold-Stressed Glycine clandestina Seedlings  
JOURNAL Unpublished (2001)  
COMMENT Contact: Singh,J.A.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-Food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: singhja@em.agr.ca.

FEATURES  
source  
1..426  
/organism="Glycine clandestina"  
/cultivar="1035"  
/db\_xref="taxon:45687"  
/clone="Gc01\_03f01"  
/clone\_1lb="Gc01\_AmFC\_ECORC\_cold\_stressed\_Glycine\_clandestina"  
/tissue\_type="Leaves, stem"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-3 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pbluescript."

BASE COUNT 116 a 92 c 86 g 125 t 7 others  
ORIGIN

Alignment Scores:  
Pred. No.: 3..92e-12 Length: 426  
Score: 172.00 Matches: 29  
Percent Similarity: 73.91% Conservative: 5  
Best Local Similarity: 63.04% Mismatches: 10  
Query Match: 62.55% Indels: 2  
DB: 12 Gaps: 1

US-10-010-731-2 (1-45) x Bg838678 (1-426)

QY 2 ThrcysGluasnleuAlaAspLysTyrArgGlyProCyspheSer-----GlyCysAsp 19  
|||||  
Db 316 ACTTGGAGAACTGCTATATACATCAGGGGTCACGTCTACCTACCGGACCTGCAT 257  
|||||

QY 20 ThrHisCysThrThrLysGluasnAlaValSerGlyArgCysArgAspAspAspAspAsp 39  
|||||  
Db 256 GATCACTGCAGAAAGATAAGAACACTTACAGCGGACGATGACGACVATTTTCGCTGH 157  
|||||

QY 40 TrpCysThrLysArgCys 45  
|||||

Db 196 TGGHGCACCAAGAAACTGT 179  
RESULT 4  
LOCUS AJ308155 517 bp mRNA linear EST 29-OCT-2001  
DEFINITION AJ308155 SSH Pisum sativum cDNA clone PSSSH1clone91, mRNA sequence.  
ACCESSION AJ308155  
VERSION AJ308155.1 GI:16507870  
KEYWORDS EST.  
SOURCE pea.  
ORGANISM Pisum sativum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

REFERENCE 1 (bases 1 to 517)  
Grunwald,U., Lapopin,L., Becker,A., Mann,P., Bomanski,K.N., Gianinazzi-Pearson,V. and Franken,P.  
Screening for genes activated in Pisum sativum mycorrhiza by arbuscule development-related expression profiling  
JOURNAL Unpublished (2001)  
COMMENT Contact: Franken P  
Biochemistry  
Max-Planck-Institute for Terrestrial Microbiology  
Marburg, Karl-von-Friesch-Strasse, D-35043, Germany.

FEATURES  
source  
1..517  
/organism="Pisum sativum"  
/cultivar="Finale"  
/db\_xref="taxon:3888"  
/clone="PSSSH1clone91"  
/clone\_1lb="SSH"  
/tissue\_type="arbuscular mycorrhiza"  
/note="minus inoculated late mutant"

BASE COUNT 161 a 87 c 102 g 167 t  
ORIGIN

Alignment Scores:  
Pred. No.: 6..86e-12 Length: 517  
Score: 171.00 Matches: 26  
Percent Similarity: 70.21% Conservative: 7  
Best Local Similarity: 55.32% Mismatches: 12  
Query Match: 62.18% Indels: 2  
DB: 9 Gaps: 1

US-10-010-731-2 (1-45) x AJ308155 (1-517)

QY 1 ArgThrCysGluasnleuAlaAspLysTyrArgGlyProCysphe-----SerGlyCys 18  
|||||  
Db 159 AAAACCTGTGAGATTTGTTGGCAGATTCAGAGGACCATCCAGATGTAATGTC 218  
|||||

QY 19 AspThrHisCysThrThrLysGluasnAlaValSerGlyArgCysArgAspAspAspAsp 38  
|||||  
Db 219 AACAAACATTGCGAGGAACAACACTTACTAGTGGAGGATGATGATTTTCGC 278  
|||||

QY 39 CysTrpCysThrLysArgCys 45  
|||||  
Db 279 TGTGTGTCACCTGAAACTGT 299  
|||||

RESULT 5  
LOCUS B0151477 574 bp mRNA linear EST 24-APR-2002  
DEFINITION B0151477 NF088A06.F1038 Developing leaf Medicago truncatula cDNA clone.  
ACCESSION B0151477  
VERSION B0151477.1 GI:2028536  
KEYWORDS EST.  
SOURCE Medicago truncatula  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliceae; Medicago.

REFERENCE	1 (bases 1 to 574)
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
JOURNAL	Unpublished (2000)
COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Insert Length: 574 Std Error: 0.00 Plate: 088 Rows: A column: 06 Seq primer: TCACACAGGAACACGCTATGAC. Location/Qualifiers
FEATURES	1..574 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF088A06LP" /clone_lib="developing leaf" /tissue_type="leaf" /dev_stage="Pooled developmental" /note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."
BASE COUNT	198 a 104 c 104 g 167 t 1 others
ORIGIN	
Alignment Scores:	
Pred. No.:	9.93e-10 Length: 574
Score:	154.50 Matches: 26
Percent Similarity:	72.34% Conservative: 8
Best Local Similarity:	55.32% Mismatches: 10
Query Match:	56.18% Indels: 3
DB:	14 Gaps: 2
US-10-010-731-2 (1-45) x BQ151477 (1-574)	
QY	1 ArgThrcGsgluAnsLeuAlaAspLysTyrArgGlyProCysPheSer-----GlyCys 18       140 AGGACTGTGTAGCATTGGCGTGAATACATACAGAGGACCATCTTCACGGAAGTAACTGCT 199 
QY	19 AsphrHrHscCysThrTrHrLysGluAsnAlaValSerGlyTyrGysATgAspAspPheArg 38       200 GATGACCACTGCACAAACAAACACACTTAATTAGTGGCAGCTGCCAT--AACTTCA 256 
QY	39 CysTrpCysThrLysArgCys 45       257 TGTTCGTGCACTCAAAACTGT 277 
Db	257 TGTTCGTGCACTCAAAACTGT 277
RESULT 6	
LOCUS	BF633403 503 bp mRNA linear EST 19-DEC-2000
DEFINITION	NF047E03DPI.F1022 Drought Medicago truncatula cDNA clone NF047E03D.F
ACCESSION	BF633403
VERSION	BF633403.1 GI:11897561
KEYWORDS	EST.
SOURCE	barrel medic.
ORGANISM	Medicago truncatula
REFERENCE	1 (bases 1 to 503)
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
JOURNAL	Unpublished (2000)
COMMENT	Contact: May GD Plant Biology Division

	The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel.: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org. Insert length: 503 Std Error: 0.00 Plate: 047 row: E column: 03 Seq primer: TCACACGAGAAACACTTATGCAC.
FEATURES	
SOURCE	Location/Qualifiers 1..503
BASE COUNT	181 a 82 c 93 g 147 t
ORIGIN	/organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF047E03DP" /clone_1lb="Drought" /tissue_type="Plantlets" /dev_stage="Pooled timepoints" /note="Vector: Lambda zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."
Pred Scores:	
Align. No.:	3.72e-08 Length: 503
Score:	141.50 Matches: 26
Percent Similarity:	70.83% Conservative: 8
Best Local Similarity:	54.17% Mismatches: 10
Query Match:	51.45% Indels: 4
DB:	Gaps: 2
US-10-010-731-2 (1-45) x BF633403 (1-503)	
OY	1 ArgThrCysGluAsnLeuAlaAspLysTyraArgGlyProCysPheSer-----GlyCys 18       Db 146 AGCACTTGTCAGCATTTGGCTGTGATCATACAGAGAGACCATCGTTCACGAGACGTAGCTGT 205     OY 19 AsphTrHisCysThrThrLysGluAsnAlaValSerGlyArg-CysArGaSpasPheAr 38              : ::      .    :   : Db 206 GATGACCACCTCCAGAACACACACACTTAATTATGTGGCACCGTCGCAT---AActTTCa 262     OY 38 GCyStrPrCysThrLysArGys 45 :   :::   :::    Db 263 ATGTTCTGCACTCAAAACTGT 284 
RESULT 7	
B1321308	366 bp mRNA linear EST 29-NOV-2001
LOCUS	saf50c11.y3 Gm-cl077 glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION	ID: Gm-cl077-2037 5' similar to SW:10KD_VIGUN P1846 10 KD PROTEIN PRECURSOR ;, mRNA sequence.
ACCESSION	B1321308
VERSION	B1321308.1 GI:15000494
KEYWORDS	EST.
SOURCE	soybean.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euariyotia; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE	1 (bases 1 to 366) Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shiu,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson.R. Public Soybean EST project Unpublished (1999)
TITLE	Contact: Shoemaker R/Public Soybean EST Project
JOURNAL	Washington University School of Medicine
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel.: 314 286 1800







Db 241 GCAACCGTGTGCCGACC---GAGAACTTTCGCCGGCCGAGTGCACACGACACGACTC 297

Qy 36 AsphearGcYstrpCysThrLysArgCys 45  
Db 298 GAGCGCAAGTGTCTACTGCGAGCGGACTGC 327

RESULT 13

LOCUS BU299919/c 485 bp mRNA linear EST 09-APR-2002

DEFINITION BU299919 Y. Ogihara unpublished cDNA library, Wh\_SL Triticum aestivum cDNA clone whs132117 3', mRNA sequence.

ACCESSION BU299919

VERSION BU299919.1 GI:20111909

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Triticum.  
1 (bases 1 to 485)  
Ogihara,Y. and Mural,K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center for Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

FEATURES

source Location/Qualifiers

1..485

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="whs132117"

/tissue\_type="seed DPA30"

/dev\_stage="Feekes" scale 11.3"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T3 Close lab at the University of California, Riverside (Akhunov, Chin , Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 99 a 143 c 139 g 102 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 0.00207 Length: 485

Score: 104.00 Matches: 21

Percent Similarity: 60.00% Conservative: 9

Best Local Similarity: 42.00% Mismatches: 14

Query Match: 37.82% Indels: 6

DB: 13 Gaps: 3

US-10-010-731-2 (1-45) x BU299919 (1-485)

Qy 1 ArgrhrcysgluansleuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18  
Db 318 CGGACGTGCGAGTGTGCAGAGCCACAGTTCAAGGCCCTCTTCAAGCAGCAGCACTGC 259

Qy 19 AspThrIscYstrpCysThrLysGluAsnAlaValSerGlyArgCysArgAsp----- 35  
Db 258 GCAACCGTGTGCCGACC---GAGAACTTTCGCCGGCCGAGTGCACACGACGACTC 202

Qy 36 AsphearGcYstrpCysThrLysArgCys 45  
Db 201 GAGCGCAAGTGTCTACTGCGAGCGGACTGC 172

RESULT 14

LOCUS BU298033/c 492 bp mRNA linear EST 09-APR-2002

DEFINITION BU298033 Y. Ogihara unpublished cDNA library, Wh\_SL Triticum aestivum cDNA clone whs123b04 3', mRNA sequence.

ACCESSION BU298033

VERSION BU298033.1 GI:20111065

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Triticum.  
1 (bases 1 to 492)  
Ogihara,Y. and Mural,K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center for Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

FEATURES

source Location/Qualifiers

1..492

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="whs123b04"

/tissue\_type="seed DPA30"

/dev\_stage="Feekes" scale 11.3"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T3 Close lab at the University of California, Riverside (Akhunov, Chin , Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 102 a 143 c 141 g 106 t

ORIGIN

Alignment Scores:

Pred. No.: 0.00211 Length: 492

Score: 104.00 Matches: 21

Percent Similarity: 60.00% Conservative: 9

Best Local Similarity: 42.00% Mismatches: 14

Query Match: 37.82% Indels: 6

DB: 13 Gaps: 3

US-10-010-731-2 (1-45) x BU298033 (1-492)

Qy 1 ArgrhrcysgluansleuAlaAspLysTyrArgGlyProCysPhe-----SerGlyCys 18  
Db 329 CGGACGTGCGAGTGTGCAGAGCCACAGTTCAAGGCCCTCTTCAAGCAGCAGCACTGC 270

Qy 19 AspThrIscYstrpCysThrLysGluAsnAlaValSerGlyArgCysArgAsp----- 35  
Db 269 GCAACCGTGTGCCGACC---GAGAACTTTCGCCGGCCGAGTGCACACGACGACTC 213

Qy 36 AsphearGcYstrpCysThrLysArgCys 45  
Db 269 GCAACCGTGTGCCGACC---GAGAACTTTCGCCGGCCGAGTGCACACGACGACTC 213



Db 212 GAGCGAAGTCTACTGCGAGCGGACTGC 183

Job time : 1052.24 secs

RESULT 15  
BG838277

LOCUS BG838277 502 bp mRNA linear EST 25-MAY-2001  
DEFINITION Gc01\_10f03\_R Gc01\_AAFc\_ECORC\_cold\_stressed\_glycine\_clandestina  
glycine clandestina cDNA clone Gc01\_10f03, mRNA sequence.

ACCESSION BG838277  
VERSION BG838277.1 GI:14204599  
KEYWORDS EST  
SOURCE Glycine clandestina.  
ORGANISM Glycine clandestina

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine  
1 (bases 1 to 502)  
Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris  
L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker  
,N.A.

REFERENCE 1  
AUTHORS Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris  
L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker  
,N.A.  
Expressed Sequence Tags from Cold-Stressed Glycine clandestina  
Seedlings  
Unpublished (2001)  
Contact: Singh,J.A.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A  
0C6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: singhja@em.agr.ca.

FEATURES  
source  
1.502  
location/Qualifiers  
/organism="Glycine clandestina"  
/cultivar="1035"  
/db\_xref="taxon:45687"  
/clone="Gc01\_10f03"  
/clone\_1lb="Gc01\_AAFc\_ECORC\_cold\_stressed\_glycine\_clandest  
ina"  
/tissue\_type="leaves, stem"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site\_1: EcoRI;  
Site\_2: XhoI; Plants incubated at 2 degrees under 12 hours  
of light/day. Harvested after only 2-3 days of cold  
treatment. cDNA was prepared with the Uni-Zap cDNA kit  
from Stratagene. Eco RI adapters were linked followed by  
digest with Xho I/Eco RI and ligated to pbluescript."

BASE COUNT 123 a 93 c 105 g 179 t 2 others  
ORIGIN

Alignment Scores:

Pred. No.: 0.00217 length: 502  
Score: 104.00 Matches: 21  
Percent Similarity: 61.22% Conservative: 9  
Best Local Similarity: 42.86% Mismatches: 13  
Query Match: 37.82% Indels: 6  
DB: 12 Gaps: 3

US-10-010-731-2 (1-45) x BG838277 (1-502)

OY 1 ArgTthCysgluAsnleuAlaAspLysTYrArgGlyProCysPheSerGlyCysAspThr 20  
|||||  
Db 104 AGAAGTTGTGAGCTCAGAGCCACGCTTCAGAGGGCGCATGTGTGAGT-----GACACC 157  
OY 21 HisCysThr-----LysGluAsnAlaValSerGlyArgCysArgAsp---Asp 36  
|||||  
Db 158 AACTGTGCTCTGTGTTGCCATACCGAAGCTTCACGTGAGAGACAATGCCGTGCTTGCCT 217  
OY 37 PheArgCysTrpCysThrLysArgCys 45  
|||||  
Db 218 CGAGATGCTCTGACACCAACAATTTGT 244

Search completed: June 21, 2003, 07:52:30

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 04:45:23 ; Search time 150 Seconds  
(without alignments)  
3753.331 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250  
Sequence: 1 GCGGATCCCAATCTAATCA.....AAAGATGTAAAGATCCCC 250

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq\_101002:\*

1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
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18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
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21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	250	19	AAV39187
2	234	93.6	507	19	AAV39195
3	232.4	93.0	490	19	AAV39186
4	179.8	71.9	200	19	AAV39190
5	169.6	67.8	293	19	AAV39191
6	156.4	62.6	468	21	AAZ49412
7	119.4	47.8	494	22	AAAD1730
8	117.8	47.1	327	19	AAV39194
9	62	24.8	62	19	AAV39196

C	10	47	18.8	47	19	AAV39197	Antifungal polypep
C	11	40.6	16.2	217	21	AAZ94226	Antifungal protein
C	12	40	16.0	141	15	AAO70126	Antimicrobial Lc-A
C	13	35.2	14.1	9542	20	AAV20260	Borrelia burgdorfe
C	14	32.2	12.9	138	14	AAO38648	Encodes antifungal
C	15	32.2	12.9	505	23	ABV12096	Human prostate exp
C	16	32.2	12.9	12138	24	ABL33942	Human immune syste
C	17	32.2	12.9	12138	24	ABK28325	DNA transcription
C	18	31.6	12.6	1809	23	AAV21125	DNA encoding novel
C	19	31.4	12.6	56583	21	AAV21125	Human low adenosin
C	20	31.4	12.6	56583	21	AAV21125	Human low adenosin
C	21	31.4	12.6	910715	20	AAV20248	Borrelia burgdorfe
C	22	31.2	12.5	37948	20	AAV20631	Photoreceptor lumin
C	23	30.8	12.3	653	22	AAH97918	Murine 7-transmem
C	24	30.8	12.3	1563	22	AAH64828	Human secreted pro
C	25	30.6	12.2	487	21	AAV38169	Arabidopsis thalia
C	26	30.6	12.2	487	24	ABK30864	Plant dwarfing/stu
C	27	30.6	12.2	502	24	ABK45283	CDNA encoding colo
C	28	30.6	12.2	620	24	ABK66218	Arabidopsis thalia
C	29	30.6	12.2	709	24	ABK30321	Human G-protein-co
C	30	30.6	12.2	1094	24	ABK49499	Sequence #101 used
C	31	30.6	12.2	1094	24	ABK30690	Plant dwarfing/stu
C	32	30.6	12.2	1636	21	AAV58012	1636 bp Candida al
C	33	30.6	12.2	1712	21	AAV57960	1712 bp Candida al
C	34	30.6	12.2	2435	23	ABV22550	Human prostate exp
C	35	30.6	12.2	2435	23	ABV25004	Human prostate exp
C	36	30.6	12.2	2435	23	ABV25302	Human prostate exp
C	37	30.6	12.2	2435	23	ABV28367	Human prostate exp
C	38	30.6	12.2	3058	22	AAH33402	Human colon cancer
C	39	30.4	12.2	1140	20	AAV58881	Human FAK-related
C	40	30.4	12.2	3791	22	AAV65534	Human focal adhesi
C	41	30.4	12.2	3791	22	AAV51382	Human focal adhesi
C	42	30.4	12.2	4052	23	ABV29192	Human prostate exp
C	43	30.4	12.2	4481	24	AAV94837	Human DNA sequence
C	44	30.2	12.1	1036	24	ABK35277	Human CDNA encodin
C	45	30.2	12.1	1122	22	AAV64478	beta-lactamase 11

#### ALIGNMENTS

AAV39187	RESULT 1
ID	AAV39187 standard; DNA; 250 BP.
AC	AAV39187;
DT	25-SEP-1998 (first entry)
DE	Alfalfa plant antifungal polypeptide ALFALFP1 encoding DNA.
XX	Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW	plant pathogenic fungus; Alfalfa; ALFALFP2; ds.
XX	Medicago sativa.
OS	Medicago sativa.
FH	Key
FT	Location/Qualifiers
FT	CD5
FT	/*tag= a
FT	/product= "mature ALFALFP1"
PN	MO9826083-AL.
PD	18-JUN-1998.
XX	
PF	11-DEC-1997; 97MO-US22662.
XX	
PR	13-DEC-1996; 96US-0766355.
XX	
PA	(MONS ) MONSANTO CO.
XX	
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;

DR WPI, 1998-348537/30.  
DR P-PSDB; AAW61964.  
XX Antifungal poly(peptide)s and genes isolated from alfalfa plant(s)  
PT - used to control plant pathogenic fungi and to produce transformed  
PT plants with increased fungal resistance  
XX Claim 3; Page 78; 97pp: English.  
XX This DNA encodes an antifungal polypeptide. Alfafp1 isolated from  
CC alfalfa plants (Medicago). The polypeptides Alfafp1 and Alfafp2 are  
CC useful to control plant fungi, especially pathogenic fungi, by  
CC transforming plant cells with a vector comprising sequences encoding  
CC Alfafp1 or Alfafp2 to allow expression of antifungally effective amounts  
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,  
CC cotton and especially potato. Micro-organisms may also be transformed  
CC to produce the polypeptides, and applied to plants to control plant  
CC fungi. The polypeptides can also be included with a suitable solvent in  
CC antifungal compositions and these can be administered to plants to  
CC control plant fungi. Such compositions and genetically engineered plants  
CC may also contain additional molecules e.g. the compositions can contain  
CC other antifungal agents or the plants contain DNA encoding insecticidal  
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful  
CC to prepare antibodies useful to detect polypeptides or isolate other  
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
CC to produce polypeptides and transgenic plants and as probes or primers in  
CC nucleic acid hybridisation e.g. to detect complementary sequences in  
CC samples, and to prepare mutants or isolate similar sequences from related  
CC species.  
XX Sequence 250 BP; 73 A; 48 C; 64 G; 65 T; 0 other:  
SQ

Query Match 100.0%; Score 250; DB 19; Length 250;  
Best Local Similarity 100.0%; Pred. No. 3.1e-73;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGATCCCAATCTAATCAACTATGAGAGAGAAATCACTAGCTGCTTATGCTTCTCT 60  
DB 1 GGGGATCCCAATCTAATCAACTATGAGAGAGAAATCACTAGCTGCTTATGCTTCTCT 60  
QY 61 TCTTGTCTCTTGTGACAAAGAAATTTGGTGACAGAGCAACCAATGTGACAAT 120  
DB 61 TCTTGTCTCTTGTGACAAAGAAATTTGGTGACAGAGCAACCAATGTGACAAT 120  
QY 121 TGGCAGATTAATATAGGGAGCATTGCTTATGCTGACACTCAGTCACAAACCAAG 180  
DB 121 TGGCAGATTAATATAGGGAGCATTGCTTATGCTGACACTCAGTCACAAACCAAG 180  
QY 181 AGACGCACTTATGAGAGGTGAGGAGCAGCTCCGCTGCTGCTACTTAAAGATGTT 240  
DB 181 AGACGCACTTATGAGAGGTGAGGAGCAGCTCCGCTGCTGCTACTTAAAGATGTT 240  
QY 241 AAGGATCCCC 250  
DB 241 AAGGATCCCC 250

RESULT 2  
AAV39195  
ID AAV39195 standard; DNA; 507 BP.  
XX  
AC AAV39195;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Antifungal polypeptide Alfafp1 mature sequence encoding DNA.  
XX  
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;  
XX plant pathogenic fungus; Alfafp1; Alfafp2; ds.  
OS Medicago sativa.  
XX  
FH Key Location/Qualifiers

FT CDS 173..310  
FT /\*tag= a  
FT /product= "mature Alfafp1"  
XX  
XX WO9826083-A1.  
XX  
XX .18-JUN-1998.  
XX  
XX .11-DEC-1997; 97MO-US22662.  
XX  
XX .13-DEC-1996; 96US-0766355.  
XX  
XX (MONS ) MONSANTO CO.  
XX  
XX Hahm S, Liang J, Rosenberger CA, Shah DM, Wu YS;  
DR WPI, 1998-348537/30.  
DR P-PSDB; AAW61964.  
XX  
XX Antifungal poly(peptide)s and genes isolated from alfalfa plant(s)  
PT - used to control plant pathogenic fungi and to produce transformed  
PT plants with increased fungal resistance  
XX Claim 5; Page 77; 97pp: English.  
XX This DNA encodes an antifungal polypeptide, Alfafp1 isolated from  
CC alfalfa plants (Medicago). The polypeptides Alfafp1 and Alfafp2 are  
CC useful to control plant fungi, especially pathogenic fungi, by  
CC transforming plant cells with a vector comprising sequences encoding  
CC Alfafp1 or Alfafp2 to allow expression of antifungally effective amounts  
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,  
CC cotton and especially potato. Micro-organisms may also be transformed  
CC to produce the polypeptides, and applied to plants to control plant  
CC fungi. The polypeptides can also be included with a suitable solvent in  
CC antifungal compositions and these can be administered to plants to  
CC control plant fungi. Such compositions and genetically engineered plants  
CC may also contain additional molecules e.g. the compositions can contain  
CC other antifungal agents or the plants contain DNA encoding insecticidal  
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful  
CC to prepare antibodies useful to detect polypeptides or isolate other  
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
CC to produce polypeptides and transgenic plants and as probes or primers in  
CC nucleic acid hybridisation e.g. to detect complementary sequences in  
CC samples, and to prepare mutants or isolate similar sequences from related  
CC species.  
XX Sequence 507 BP; 181 A; 85 C; 102 G; 136 T; 3 other:  
SQ

Query Match 93.6%; Score 234; DB 19; Length 507;  
Best Local Similarity 100.0%; Pred. No. 8.9e-68;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAATCTAATCAACTATGAGAGAAATCAGTACGCTTATGCTTCTCTCTTCTGTT 68  
DB 77 CAATCTAATCAACTATGAGAGAAATCAGTACGCTTATGCTTCTCTCTTCTGTT 136  
QY 69 CTCTTTGTTGACAGAAATTTGTGTGACAGAGCAGAAATGTGAGATTTGGCAGAT 128  
DB 137 CTCTTTGTTGACAGAAATTTGTGTGACAGAGCAGAAATGTGAGATTTGGCAGAT 196  
QY 129 AATATAGGGAGCATTGCTTATGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 188  
DB 197 AATATAGGGAGCATTGCTTATGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 256  
QY 189 GTTATGAGAGGTGAGAGCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242  
DB 257 GTTATGAGAGGTGAGAGCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310

RESULT 3  
AAV39186  
ID AAV39186 standard; DNA; 490 BP.  
XX

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AC AAV39186;
XX 01-OCT-1998 (first entry)
XX
DE Antifungal polypeptide AlfaFP1 encoding cDNA.
XX
KM Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ss.
XX
OS Medicago sativa.
XX
XX Key Location/Qualifiers
XX CDS 75..293
XX FT /*tag= a
XX FT /transl_except= (pos:129..131, aa:Glu)
XX FT sig_peptide 75..155
XX FT /*tag= b
XX FT mat_peptide 156..290
XX FT /*tag= c
XX
XX MO9826083-A1.
XX
XX 18-JUN-1998.
XX
XX 11-DEC-1997; 97WO-US22662.
XX
XX 13-DEC-1996; 96US-0766355.
XX
XX (MONS ) MONSANTO CO.
XX
XX Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX WPI: 1998-348537/30.
XX P-PSDB: AAM61967.
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
XX - used to control plant pathogenic fungi and to produce transformed
XX plants with increased fungal resistance
XX
XX Claim 5; Fig 1; 97pp: English.
XX
XX This cDNA encodes an antifungal polypeptide, AlfaFP1 isolated from
XX alfalfa plants (Medicago). The polypeptides AlfaFP1 and AlfaFP2 are
XX useful to control plant fungi, especially pathogenic fungi, by
XX transforming plant cells with a vector comprising sequences encoding
XX AlfaFP1 or AlfaFP2 to allow expression of antifungally effective amounts
XX of the polypeptide. Such transformed plants may be e.g. apple, wheat,
XX cotton and especially potato. Micro-organisms may also be transformed
XX to produce the polypeptides, and applied to plants to control plant
XX fungi. The polypeptides can also be included with a suitable solvent in
XX antifungal compositions and these can be administered to plants to
XX control plant fungi. Such compositions and genetically engineered plants
XX may also contain additional molecules e.g. the compositions can contain
XX other antifungal agents or the plants contain DNA encoding insecticidal
XX (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
XX to prepare antibodies useful to detect polypeptides or isolate other
XX alfalfa plant antifungal protein antigens. The nucleic acids are useful
XX to produce polypeptides and transgenic plants and as probes or primers in
XX nucleic acid hybridisation e.g. to detect complementary sequences in
XX samples, and to prepare mutants or isolate similar sequences from related
XX species.
XX
XX Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other:
XX
XX Query Match 93.0%; Score 232.4; DB 19; Length 490;
XX Best Local Similarity 99.6%; Pred. No. 3e-67;
XX Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 9 CAATCTATCAACATGATGAGAGAAATCAGTGGCTTATGCTTCTCTTGGT 68
XX ||||||||||||||||||||||||||||||||||||||||||||||||
XX 60 CAATCTATCAACATGATGAGAGAAATCAGTGGCTTATGCTTCTCTTGGT 119

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OY 69 CTCCTTGTGACAGAAATTTGCTGACAGAGCCAGAAACATGTGAGAAATTTGGCAGAT 128
XX ||||||||||||||||||||||||||||||||||||||||||||||||
DB 120 CTCCTTGTGACAGAAATTTATGCTGACAGAGCCAGAAACATGTGAGAAATTTGGCAGAT 179
OY 129 AATATAGGGGACCATGCTTTTATGCTGTGTGACACTGACAGCAACCAAGAGACCA 188
XX ||||||||||||||||||||||||||||||||||||||||||||||||
DB 180 AATATAGGGGACCATGCTTTTATGCTGTGTGACACTGACAGCAACCAAGAGACCA 239
OY 189 GTTACTGGAAGGTGTAGGACGACTTCCGCTGCTGTACTTAAAGATGTTAA 242
XX ||||||||||||||||||||||||||||||||||||||||||||||||
DB 240 GTTACTGGAAGGTGTAGGACGACTTCCGCTGCTGTACTTAAAGATGTTAA 293
XX
XX RESULT 4
XX AAV39190
XX ID AAV39190 standard; DNA; 200 BP.
XX
XX AAV39190;
XX
XX 25-SEP-1998 (first entry)
XX
XX Antifungal polypeptide AlfaFP2 5' region.
XX
XX Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX
XX Medicago sativa.
XX
XX MO9826083-A1.
XX
XX 18-JUN-1998.
XX
XX 11-DEC-1997; 97WO-US22662.
XX
XX 13-DEC-1996; 96US-0766355.
XX
XX (MONS ) MONSANTO CO.
XX
XX Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX WPI: 1998-348537/30.
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
XX - used to control plant pathogenic fungi and to produce transformed
XX plants with increased fungal resistance
XX
XX Claim 18; Page 75; 97pp: English.
XX
XX This sequence represents the 5' region of the DNA encoding an antifungal
XX polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The
XX polypeptides AlfaFP1 and AlfaFP2 are useful to control plant fungi,
XX especially pathogenic fungi, by transforming plant cells with a vector
XX comprising sequences encoding AlfaFP1 or AlfaFP2 to allow expression of
XX antifungally effective amounts of the polypeptide. Such transformed
XX plants may be e.g. apple, wheat, cotton and especially potato.
XX Micro-organisms may also be transformed to produce the polypeptides, and
XX applied to plants to control plant fungi. The polypeptides can also be
XX included with a suitable solvent in antifungal compositions and these can
XX be administered to plants to control plant fungi. Such compositions and
XX genetically engineered plants may also contain additional molecules e.g.
XX the compositions can contain other antifungal agents or the plants
XX contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
XX proteins. The polypeptides are also useful to prepare antibodies useful
XX to detect polypeptides or isolate other alfalfa plant antifungal protein
XX antigens. The nucleic acids are useful to produce polypeptides and
XX transgenic plants and as probes or primers in nucleic acid hybridisation
XX e.g. to detect complementary sequences in samples, and to prepare mutants
XX or isolate similar sequences from related species.
XX
XX Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other:
XX
XX Query Match 71.9%; Score 179.8; DB 19; Length 200;
XX Best Local Similarity 98.9%; Pred. No. 6.9e-50;
XX

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CC recombinant expression system, capable of transforming plants like,  
CC Canola (Brassica napus), under the constitutive control of CamV 35S  
CC inducible promoter, responsive to pathogen infections. T-DNA sequence is  
CC also present, for integration of the expression system into the plant  
CC genome. Transgenic plants expressing DR206 and defensin protein,  
CC inhibited fungal growth in-vitro and are resistant to pathogenic  
CC infections of Rhizoctonia solani, Leptosphaeria maculans and Sclerotinia  
CC sclerotiorum.  
XX  
XX  
SQ Sequence 468 BP; 153 A; 88 C; 84 G; 143 T; 0 other;  
  
Query Match 62.6%; Score 156.4; DB 21; Length 468;  
Best Local Similarity 80.0%; Pred. No. 6.2e-42;  
Matches 184; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
  
OY 13 CTAATCAAACTATGAGAAATATCATCTAGCTGGCTTATGCTTCTCTTGGTCTCT 72  
DB 67 CTTAAGAACCCATGGAGAGAAATACCTAGCTTGTCTTCTCTCTCTCTCTCTCT 126  
OY 73 TTGTTGCACAGAAATTTGTGTGACAGAGCCAGAACATGAGATTTGGCAGATAAT 132  
DB 127 TTGTTGCACAGAAATAGTGAGTGAAGCAACATGATGAGATTTGGCTGTTCA 186  
OY 133 ATAGGGGACCATGCTTTAGTGTGTGACACTCTGCAACAAAGAGAGAGCAGTTA 192  
DB 187 ATAGGGGAGTATGCTTCGCTGATGACCGCTCAGTGTGATGACACAGAGCGCGCAATTA 246  
OY 193 GTGGAAGGTATGGGACGACCTCCGCTGGTGTACTAAAGATGTAA 242  
DB 247 GCGGCAAGATGACAGGATGACTTTCGCTGTGGTGACATAAAGCTTTAA 296  
  
RESULT 7  
AAD17530  
ID AAD17530 standard; cDNA: 494 BP.  
XX  
AC AAD17530;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
DE Soybean Gly m2 protein encoding cDNA from clone sls1c.pk027.a11.  
XX  
KM Soybean: allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1;  
KM Soybean vacuolar protein; Gly m 1A; Gly m 1B; rGly m3; Glycinin G1;  
KM alab1b; food; infant formula; animal feed; coating; salad oil; syrup;  
KM spraying oil; roasting oil; frying oil; cracker; confectionery product;  
KM snack food; topping; sauce; batter; bread; baking mixture; dough;  
KM Gly m2 protein; clone sls1c.pk027.a11; ss.  
XX  
OS Glycine max.  
XX  
FH  
FH  
FT CDS Location/Qualifiers  
FT 46..273  
FT /\*tag= a  
FT /product= "Soybean Gly m2 protein"  
XX  
PN WO200168887-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 15-MAR-2001; 2001WO-US08254.  
XX  
PR 16-MAR-2000; 2000US-0189823.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Jung R, Kinney AJ;  
XX  
DR WPI; 2001-582460/65.  
XX P-PSDB; AAEI0361.  
XX  
PT Recombinant expression construct to lower allergen (e.g. Gly m Bd 30K)

PT content of a soybean, comprises a nucleic acid fragment encoding the  
PT allergen, useful for producing soybean plants which can be used to make  
PT soybean products  
XX  
XX  
PS Example 7; Page 51-52; 57pp; English.  
XX  
CC The patent discloses hypoallergenic transgenic soybeans and recombinant  
CC expression constructs to lower soybean vacuolar protein, commonly known  
CC as P34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m 1A,  
CC Gly m 1B, rGly m3 or Glycinin G1 (alab1b). The allergen content of the  
CC soybean is reduced by sense suppression which is accomplished by using  
CC the expression construct that comprises a nucleic acid fragment encoding  
CC the allergen. The constructs are useful for producing hypoallergenic  
CC transgenic soybean plants which can be used to make hypoallergenic  
CC soybean products which can be used in a variety of food (e.g. infant  
CC formulae) and animal feed applications. The oil made from seeds of the  
CC hypoallergenic transgenic soybean plants can be used as ingredients,  
CC as coatings, as salad oils, as spraying oils, as roasting oils, and  
CC as frying oils. The foods in which the oil may be used include crackers  
CC and snack foods, confectionery products, syrups and toppings, sauces,  
CC batter and bread; mixtures, baking mixes and doughs. The present  
CC sequence is soybean Gly m2 protein encoding cDNA from sls1c.pk027.a11  
CC clone. This sequence is a minor soybean seed allergen.  
XX  
SQ Sequence 494 BP; 153 A; 97 C; 103 G; 134 T; 7 other;  
  
Query Match 47.8%; Score 119.4; DB 22; Length 494;  
Best Local Similarity 74.9%; Pred. No. 1.3e-29;  
Matches 179; Conservative 0; Mismatches 51; Indels 9; Gaps 2;  
  
OY 13 CTAATCAAACTATGAGAAATATCATCTAGCTGGCTTATGCTTCTCTTGGTCTCT 72  
DB 35 CTAATTAAGCCATGGAGAGAAATATCATAGCTGTGTGCTTCTCTCTCTCTCTCT 94  
OY 73 TTGTTGCACAGAAATTTGTGTGACAGAGCCAGAACATGAGATTTGGCAGATA 129  
DB 95 TTGTTGCTCAAGAGATTGTGTGCAAACTGAGCAAAAGACTTCCGAGAACCTGGCAGATA 154  
OY 130 AATATAGGGGACCATGCTT-----TAGTGTGTGTGACACTGACCTGCAACCAAGAGCA 183  
DB 155 CATACAGGGGTCATCTCTTCCACCACTGCGCACTGCGATGATCACTGCAAGACAAAGAGC 214  
OY 184 AGCAGCTTAGTGAGAGAGTGTAGGAGCACTTCGCTGCTGTGTACTAAAGATGTAA 242  
DB 215 ACTTGTCTAGAGGACAGATGAGGAGGAGATTTGCTGTGTGTCACCAAAACTGTAA 273  
  
RESULT 8  
AAV39194  
ID AAV39194 standard; DNA: 327 BP.  
XX  
AC AAV39194;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Antifungal polypeptide AlfAFP2 3' region.  
XX  
KM Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;  
KM plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.  
XX  
OS Medicago sativa.  
XX  
PN WO9826083-A1.  
XX  
PD 18-JUN-1998.  
XX  
PF 11-DEC-1997; 97WO-US22662.  
XX  
PR 13-DEC-1996; 96US-0766355.  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;

XX DR WPI: 1998-348537/30.  
XX XX  
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)  
PT - used to control plant pathogenic fungi and to produce transformed  
PT plants with increased fungal resistance  
PS  
PS Claim 18: Page 77; 97pp: English.  
XX  
XX This sequence represents the 3' region of the DNA encoding an antifungal  
CC polypeptide. AlfAFP2 isolated from alfalfa plants (Medicago). The  
CC polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,  
CC especially pathogenic fungi, by transforming plant cells with a vector  
CC comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of  
CC antifungally effective amounts of the polypeptide. Such transformed  
CC plants may be e.g. apple, wheat, cotton and especially potato.  
CC Micro-organisms may also be transformed to produce the polypeptides, and  
CC applied to plants to control plant fungi. The polypeptides can also be  
CC included with a suitable solvent in antifungal compositions and these can  
CC be administered to plants to control plant fungi. Such compositions and  
CC genetically engineered plants may also contain additional molecules e.g.  
CC the compositions can contain other antifungal agents or the plants  
CC contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*)  
CC proteins. The polypeptides are also useful to prepare antibodies useful  
CC to detect polypeptides or isolate other alfalfa plant antifungal protein  
CC antigens. The nucleic acids are useful to produce polypeptides and  
CC transgenic plants and as probes or primers in nucleic acid hybridisation  
CC e.g. to detect complementary sequences in samples, and to prepare mutants  
CC or isolate similar sequences from related species.  
XX  
XX Sequence 327 BP: 125 A; 49 C; 60 G; 91 T; 2 other;  
SQ

Query Match 47.1%; Score 117.8; DB 19; Length 327;  
Best Local Similarity 94.6%; Pred. No. 3.9e-29;  
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 114 GAGATTTGGCAGATTAATATAGGGACCATGCTTAGTGTTGGACACTACGCACA 173  
DB 1 GAGATTTTGGCGGATTAAGTATAGGGACCATGCTTAGTGTTGGACACTACGCACA 60  
QY 174 ACCAAGAGACGACGCTTAGTGGAAGGTGTAGGGAGACCTTCGGCGTGGCTACTATA 233  
DB 61 ACCAAGAGACGACGCTTAGTGGAAGGTGTAGGGAGACCTTCGGCTTAGTGCTACTATA 120

QY 234 AGATGTTAA 242  
DB 121 AGATGTTAA 129

RESULT 9  
AAV39196  
ID AAV39196 standard; DNA: 62 BP.  
XX  
AC AAV39196;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Antifungal polypeptide AlfAFP2 5' gene specific primer.  
XX  
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;  
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; PCR primer; ss.  
XX  
XX Synthetic.  
OS Medicago sativa.  
XX  
PN WO9826083-A1.  
XX  
PD 18-JUN-1998.  
XX  
PF 11-DEC-1997; 97WO-US22662.  
XX  
PR 13-DEC-1996; 96US-0766355.  
XX

PA (MONS ) MONSANTO CO.  
XX  
XX Hakiimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;  
PI WPI: 1998-348537/30.  
XX  
XX  
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)  
PT - used to control plant pathogenic fungi and to produce transformed  
PT plants with increased fungal resistance  
PS  
PS Example 4: Page 78; 97pp: English.  
XX  
XX This primer is used for the PCR amplification of the cDNA encoding an  
CC antifungal polypeptide, AlfAFP2. The antifungal polypeptides AlfAFP1 and  
CC AlfAFP2 isolated from alfalfa plants (Medicago) are useful to control  
CC plant fungi, especially pathogenic fungi, by transforming plant cells  
CC with a vector comprising sequences encoding AlfAFP1 or AlfAFP2 to allow  
CC expression of antifungally effective amounts of the polypeptide. Such  
CC transformed plants may be e.g. apple, wheat, cotton and especially  
CC potato. Micro-organisms may also be transformed to produce the  
CC polypeptides, and applied to plants to control plant fungi. The  
CC polypeptides can also be included with a suitable solvent in antifungal  
CC compositions and these can be administered to plants to control plant  
CC fungi. Such compositions and genetically engineered plants may also  
CC contain additional molecules e.g. the compositions can contain other  
CC antifungal agents or the plants contain DNA encoding insecticidal  
CC (e.g. *Bacillus thuringiensis*) proteins. The polypeptides are also useful  
CC to prepare antibodies useful to detect polypeptides or isolate other  
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
CC to produce polypeptides and transgenic plants and as probes or primers in  
CC nucleic acid hybridisation e.g. to detect complementary sequences in  
CC samples, and to prepare mutants or isolate similar sequences from related  
CC species.  
XX  
XX Sequence 62 BP: 18 A; 15 C; 12 G; 17 T; 0 other;  
SQ

Query Match 24.8%; Score 62; DB 19; Length 62;  
Best Local Similarity 100.0%; Pred. No. 7.6e-11;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGATCCCAATCTATATCAAACTATGAGAGAAATCACTACTGCTTATCTTCCT 60  
DB 1 GGGGATCCCAATCTATATCAAACTATGAGAGAAATCACTACTGCTTATCTTCCT 60

QY 61 TC 62  
DB 61 TC 62

RESULT 10  
AAV39197/c  
ID AAV39197 standard; DNA: 47 BP.  
XX  
AC AAV39197;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Antifungal polypeptide AlfAFP2 3' gene specific primer.  
XX  
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;  
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; PCR primer; ss.  
XX  
XX Synthetic.  
OS Medicago sativa.  
XX  
PN WO9826083-A1.  
XX  
PD 18-JUN-1998.  
XX  
PF 11-DEC-1997; 97WO-US22662.  
XX  
PR 13-DEC-1996; 96US-0766355.  
XX



PA (MONS ) MONSANTO CO.  
 XX  
 PI Hakim S, Liang J, Rosenberger CA, Shah DM, Wu YS;  
 XX WPI; 1998-348537/30.  
 DR  
 XX  
 PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)  
 PT - used to control plant pathogenic fungi and to produce transformed  
 PT plants with increased fungal resistance  
 PS  
 XX Example 4; Page 78; 97pp; English.  
 CC This primer is used for the PCR amplification of the cDNA encoding an  
 CC antifungal polypeptide, AlfAFP2. The antifungal polypeptides AlfAFP1 and  
 CC AlfAFP2 isolated from alfalfa plants (Medicago) are useful to control  
 CC plant fungi, especially pathogenic fungi, by transforming plant cells  
 CC with a vector comprising sequences encoding AlfAFP1 or AlfAFP2 to allow  
 CC expression of antifungally effective amounts of the polypeptide. Such  
 CC transformed plants may be e.g. apple, wheat, cotton and especially  
 CC potato. Micro-organisms may also be transformed to produce the  
 CC polypeptides, and applied to plants to control plant fungi. The  
 CC polypeptides can also be included with a suitable solvent in antifungal  
 CC compositions and these can be administered to plants to control plant  
 CC fungi. Such compositions and genetically engineered plants may also  
 CC contain additional molecules e.g. the compositions can contain other  
 CC antifungal agents or the plants contain DNA encoding insecticidal  
 CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful  
 CC to prepare antibodies useful to detect polypeptides or isolate other  
 CC alfalfa plant antifungal protein antigens. The nucleic acids are useful  
 CC to produce polypeptides and transgenic plants and as probes or primers in  
 CC nucleic acid hybridisation e.g. to detect complementary sequences in  
 CC samples, and to prepare mutants or isolate similar sequences from related  
 CC species.  
 XX  
 SO Sequence 47 BP; 11 A; 13 C; 11 G; 12 T; 0 other;  
 Query Match 18.8%; Score 47; DB 19; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 204 AGGAGACACTTCGCTGCTGCTACTAAAGATTAAAGATCCCC 250  
 DB 47 AGGAGACACTTCGCTGCTGCTGCTACTAAAGATTAAAGATCCCC 1  
 RESULT 11  
 ID AA294226 standard; DNA: 217 BP.  
 XX  
 AC AA294226;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Antifungal protein TfeAFP synthetic gene.  
 KW TfeAFP1; antifungal; fungicide; tall fescue; transgenic plant;  
 KW crop protection; disease resistance; biological control; PAPF1; ss.  
 OS Chimeric - Petunia hybrida.  
 OS Chimeric - Festuca arundinacea.  
 XX  
 PN WO200011178-A2.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 18-AUG-1999; 99WO-US18866.  
 XX  
 PR 19-AUG-1998; 98US-0097150.  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Liang J, Miltanck C, Wu Y, Shah D;  
 XX

DR WPI; 2000-246567/21.  
 XX  
 PT Novel nucleic acid encoding Festuca plant antifungal polypeptide useful  
 PT for producing transgenic plants having resistance to fungal disease  
 XX  
 XX  
 PS Example 4; Page 88; 90pp; English.  
 CC The present sequence is that of a synthetic gene encoding a fusion  
 CC between the signal peptide of the petunia antifungal protein PAPF1  
 CC and novel fescue antifungal protein TfeAFP1 mature polypeptide (see  
 CC AAY79227). The gene was designed for expression in potato. It was  
 CC constructed by PCR amplification (see AA294221-25). TfeAFP1 shows  
 CC antifungal activity against Fusarium and Verticillium, and is 1 of  
 CC 9 novel antifungal proteins (see AAY79227-35) isolated from fescue  
 CC seed. Claimed nucleic acids encoding TfeAFP proteins can be cloned  
 CC into vectors for transformation of plant-colonizing microorganisms  
 CC or plants, thereby providing a method of inhibiting fungal growth  
 CC on plants. The proteins can also be formulated into compositions  
 CC useful in controlling undesired fungi.  
 XX  
 SO Sequence 217 BP; 52 A; 31 C; 53 G; 81 T; 0 other;  
 Query Match 16.2%; Score 40.6; DB 21; Length 217;  
 Best Local Similarity 60.4%; Pred. No. 0.0017;  
 Matches 84; Conservative 0; Mismatches 54; Indels 1; Gaps 1;  
 OY 1 GGGATCCCAATCTATCAAACTATG-GAGAAAGAACTAGCTGGCTTATGCTCTC 59  
 DB 1 GGGATCCCAATCTATCAAACTATGAGATATTTCTTTCTTATTTCTTCTTCTC 60  
 OY 60 TTCTTGCTCTCTTTGTCACAAAGAAATTTGCTGACGAGACCAACATGTGAGAT 119  
 DB 61 TTTTGCTTACTACTCTTCTTACCTCAGCTCTATGTCGAGTGAAGAGATGTGAGTGCAC 120  
 OY 120 TTGGCAGTAAATATATAGG 138  
 DB 121 TTTGTTCTCTAGATATCG 139  
 RESULT 12  
 ID AAQ70126 standard; cDNA: 141 BP.  
 XX  
 AC AAQ70126;  
 XX  
 DT 14-FEB-1995 (first entry)  
 XX  
 DE Antimicrobial Lc-AFP.  
 KW Antimicrobial; Lc-AFP; symbiosis; disease-resistance;  
 KW fungus-resistance; Clavibacter xyli subsp. cynodortii; Cxc;  
 KW crop improvement; endophyte; ss.  
 OS Lathyrus cicerca.  
 XX  
 PN WO9416076-A.  
 XX  
 PD 21-JUL-1994.  
 XX  
 PF 05-JAN-1994; 94WO-GB00012.  
 XX  
 PR 08-JAN-1993; 93GB-0000281.  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Dubock AC, Powell KA, Rees SB;  
 XX  
 DR WPI; 1994-249223/30.  
 DR P-PSDB; AAR57322.  
 XX  
 PT Antimicrobial protein producing endo-symbiotic microorganisms -  
 PT is produced by combining nucleic acids encoding the protein with  
 PT an endophyte, useful for protecting plant hosts from esp. fungal



SQ Sequence 138 BP; 43 A; 30 C; 32 G; 33 T; 0 other;

Query Match 12.9%; Score 32.2; DB 14; Length 138;  
 Best Local Similarity 58.8%; Pred. No. 0.9;  
 Matches 77; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

QY 108 ACATGTGAGAAATTTGGCAGATTAATATAGGAGCAGCTTGTAGTGT-----TGTGAC 161  
 4 ACTTGCAGAACTTTCTGAGCTTTCAGAGGACCATGATTCAGATGGAAGCTGCAC 63

DB 162 ACTGCTGACACACCAAGAGAGCAGCTTGTAGTGTAGGAGCAGCTTCCGCTGC 221  
 64 AAGCATTTGAGAAAGACAGCATCTTCTTGTGAAAGATGCAAGATGATTTCTGCTGG 123

QY 222 TGGTGTACTAA 232  
 124 TGCCTAGTAA 134

DB 124 TGCCTAGTAA 134

RESULT 15  
 ABV12096  
 ID ABV12096 standard; cDNA; 505 BP.  
 XX  
 AC ABV12096;  
 XX  
 DT 13-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 12087.  
 XX  
 KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI: 2001-662795/76.  
 XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer  
 XX  
 PS Claim 1; Page 1983; 11750pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 SX  
 SQ Sequence 505 BP; 146 A; 97 C; 81 G; 181 T; 0 other;

Query Match 12.9%; Score 32.2; DB 23; Length 505;  
 Best Local Similarity 50.3%; Pred. No. 1.5;  
 Matches 79; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 60 TTCTTGCTCTCTTTGTCAGAGAAATTTGTGTCAGAGCAGAGCAGATGTGAGAT 119  
 328 TTCTTGCGCTTTTGGCTCCAGAGCAATTTACTTAACAGGCTAAATGTTGGGAAT 387

DB 120 TTGGCAGATTAATATATAGGAGCAGCTTGTAGTGTGTGACACTGCACACCAAA 179  
 388 TTCTCTTGCGGTTTATGAAATTTTATTTTATTTTAAATTTTAAAGCATAACCAAA 447

QY 180 GAGACGCACTTGTGAAAGGTGTAGGACGACTTCC 216  
 448 AAATTTACCACTTTAGAAAAGTTAGGCTTCCCTGC 484

DB 448 AAATTTACCACTTTAGAAAAGTTAGGCTTCCCTGC 484

Search completed: June 21, 2003, 05:36:24  
 Job time : 152 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 05:14:43 ; Search time 40 Seconds  
(without alignments)  
1916.730 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250  
Sequence: 1 GGGGATCCCAATCTATCA.....AAAGATGTTAAGATCCCC 250

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/lna/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PC105\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/Backfile1.seq:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	250	3	US-08-766-355-13
2	250	100.0	250	4	US-09-003-198A-13
3	250	100.0	250	4	US-09-428-805-13
4	234	93.6	490	4	US-09-003-198A-19
5	234	93.6	507	4	US-08-766-355-10
6	234	93.6	507	4	US-09-003-198A-10
7	234	93.6	507	4	US-09-428-805-10
8	181.2	72.5	189	4	US-09-003-198A-18
9	179.8	71.9	200	3	US-08-766-355-5
10	179.8	71.9	200	4	US-09-003-198A-5
11	179.8	71.9	200	4	US-09-428-805-5
12	169.6	67.8	293	4	US-08-766-355-6
13	169.6	67.8	293	4	US-09-003-198A-6
14	169.6	67.8	293	4	US-09-428-805-6
15	117.8	47.1	327	3	US-08-766-355-9
16	117.8	47.1	327	4	US-09-003-198A-9
17	117.8	47.1	327	4	US-09-428-805-9
18	62	24.8	62	3	US-08-766-355-11
19	62	24.8	62	4	US-09-003-198A-11
20	62	24.8	62	4	US-09-428-805-11
21	47	18.8	47	3	US-08-766-355-12
22	47	18.8	47	4	US-09-003-198A-12
23	47	18.8	47	4	US-09-428-805-12
24	40	16.0	141	1	US-08-377-687-35
25	40	16.0	141	1	US-08-777-192-35
26	40	16.0	141	4	US-08-971-982-35
27	31.2	12.5	37948	4	US-09-251-645-11

28	30.6	12.2	709	4	US-09-280-116-91	Sequence 91, Appl
29	30.4	12.2	3791	3	US-09-377-310-1	Sequence 1, Appl
30	29.8	11.9	1102	2	US-08-132-990A-1	Sequence 1, Appl
31	29.8	11.9	1102	5	PCR-US92-09382-1	Sequence 1, Appl
32	29.8	11.9	1307	2	US-08-867-030B-6	Sequence 6, Appl
33	29.8	11.9	1307	2	PCR-US95-06119-6	Sequence 6, Appl
34	29.8	11.9	1819	1	US-08-487-753-6	Sequence 6, Appl
35	29.8	11.9	1819	2	US-08-480-065-6	Sequence 6, Appl
36	29.8	11.9	1819	3	US-08-487-744-6	Sequence 6, Appl
37	29.8	11.9	1819	5	PCR-US93-09167-6	Sequence 6, Appl
38	29.8	11.9	2157	2	US-08-132-990A-7	Sequence 6, Appl
39	29.8	11.9	2157	5	PCR-US92-09382-7	Sequence 7, Appl
40	29.8	11.9	2554	2	US-08-627-254C-28	Sequence 28, Appl
41	29.2	11.7	948	3	US-09-135-639-3	Sequence 3, Appl
42	29.2	11.7	1215	2	US-09-092-770-8	Sequence 8, Appl
43	29.2	11.7	1215	4	US-09-222-851-8	Sequence 8, Appl
44	29	11.6	984	4	US-09-134-001C-2705	Sequence 2705, Ap
45	29	11.6	1400	3	US-09-191-099-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-766-355-13  
Sequence 13, Application US/08766355  
Patent No. 6121436  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakim, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,355  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-766-355-13  
  
Query Match 100.0% Score 250; DB 3; Length 250;  
Best Local Similarity 100.0% Pred. No. 9.2e-76;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GGGATCCCAATCTATCAACTATGAGAGCAATCACTAGCTGCTTATGCTTCCCT 60  
|||||

Db 1 GGGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCCCTCT 60  
QY TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTACAGAGCCAGAACTATGTGAATTT 120  
Db 61 TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTACAGAGCCAGAACTATGTGAATTT 120  
QY 121 TGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGACACCTCAGCAACCAAG 180  
Db 121 TGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGACACCTCAGCAACCAAG 180  
QY 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGGTGTACTAAAGATGTT 240  
Db 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGGTGTACTAAAGATGTT 240  
QY 241 AAGGATCCCC 250  
Db 241 AAGGATCCCC 250

## RESULT 2

US-09-003-198A-13  
: Sequence 13, Application US/09003198A  
: Patent No. 6316407  
: GENERAL INFORMATION:  
: APPLICANT: Liang, Jihong  
: APPLICANT: Shah, Dilip Meghania  
: APPLICANT: Wu, Yonnie S.  
: APPLICANT: Rosenberger, Cindy A.  
: APPLICANT: Hakim, Salim  
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
: NUMBER OF SEQUENCES: 19  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold White & Durkee  
: STREET: P. O. Box 4433  
: CITY: Houston  
: STATE: Texas  
: COUNTRY: USA  
: ZIP: 77210  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/003.198A  
: FILING DATE: 07-JAN-1998  
: CLASSIFICATION:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Patterson, Melinda L.  
: REGISTRATION NUMBER: 33,062  
: REFERENCE/DOCKET NUMBER: MOBT.193  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (713) 787-1400  
: TELEFAX: (713) 787-1440  
: INFORMATION FOR SEQ ID NO: 13:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 250 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
US-09-003-198A-13

Query Match 100.0%; Score 250; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. NO. 9.2e-76;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCCCTCT 60  
Db 1 GGGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCCCTCT 60  
QY 61 TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120  
Db 61 TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120

Db 61 TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120  
QY 121 TGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGACACCTCAGCAACCAAG 180  
Db 121 TGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGACACCTCAGCAACCAAG 180  
QY 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGGTGTACTAAAGATGTT 240  
Db 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGCAGCTCCGCTGGTGTACTAAAGATGTT 240  
QY 241 AAGGATCCCC 250  
Db 241 AAGGATCCCC 250

## RESULT 3

US-09-428-805-13  
: Sequence 13, Application US/09428805  
: Patent No. 6329504  
: GENERAL INFORMATION:  
: APPLICANT: Liang, Jihong  
: APPLICANT: Shah, Dilip Meghania  
: APPLICANT: Wu, Yonnie S.  
: APPLICANT: Rosenberger, Cindy A.  
: APPLICANT: Hakim, Salim  
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
: NUMBER OF SEQUENCES: 14  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 77210  
: CITY: Houston  
: STATE: Texas  
: COUNTRY: United States of America  
: ZIP: 77210  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/428.805  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/766,355  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Kitchell, Barbara S.  
: REGISTRATION NUMBER: 33,928  
: REFERENCE/DOCKET NUMBER: MOBT.063  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (512) 418-3000  
: TELEFAX: (512) 474-7577  
: INFORMATION FOR SEQ ID NO: 13:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 250 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
US-09-428-805-13

Query Match 100.0%; Score 250; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. NO. 9.2e-76;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCCCTCT 60  
Db 1 GGGGATCCCAATCTAATCAAACTATGAGAGAAATCAGCTGGCTTATGCTTCCCTCT 60  
QY 61 TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120  
Db 61 TCTTGTTCTCTCTTTGTTGTCACAGAAATTTGTGTGACAGAGCCAGAACTATGTGAATTT 120

QY	121	TGGCAGATAAATATATGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACACCAAAAG	180
Db	121	TGGCAGATAAATATATGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACACCAAAAG	180
QY	181	AGAACGCGTAGTGTGAAGGTGTAGGAGCAGACTTCGCGTGTGTACTAAAGATGTT	240
Db	181	AGAACGCGTAGTGTGAAGGTGTAGGAGCAGACTTCGCGTGTGTGTACTAAAGATGTT	240
QY	241	AAGGATCCCC	250
Db	241	AAGGATCCCC	250

	RESULT 4	
	US-09-003-198A-19	
	: Sequence 19, Application US/09003198A	
	: Patent No. 6316407	
	: GENERAL INFORMATION:	
	: APPLICANT: Liang, Jihong	
	: APPLICANT: Shah, Dilip Maganlal	
	: APPLICANT: Wu, Yonnie S.	
	: APPLICANT: Rosenberger, Cindy A.	
	: APPLICANT: Hakim, Salim	
	: TITLE OF INVENTION: Antifungal Polypeptide and Methods for	
	: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi	
	: NUMBER OF SEQUENCES: 19	
	: CORRESPONDENCE ADDRESS:	
	: ADDRESSEE: Arnold White & Durkee	
	: STREET: P. O. Box 4433	
	: CITY: Houston	
	: STATE: Texas	
	: COUNTRY: USA	
	: ZIP: 77210	
	: COMPUTER READABLE FORM:	
	: MEDIUM TYPE: Floppy disk	
	: COMPUTER: IBM PC compatible	
	: OPERATING SYSTEM: PC-DOS/MS-DOS	
	: SOFTWARE: Patentin Release #1.0, Version #1.30	
	: CURRENT APPLICATION DATA:	
	: APPLICATION NUMBER: US/09/003.198A	
	: FILING DATE: 07-JAN-1998	
	: CLASSIFICATION:	
	: ATTORNEY/AGENT INFORMATION:	
	: NAME: Patterson, melinda L.	
	: REGISTRATION NUMBER: 33,062	
	: REFERENCE/DOCKET NUMBER: MOBT:193	
	: TELECOMMUNICATION INFORMATION:	
	: TELEPHONE: (713) 787-1400	
	: TELEFAX: (713) 787-1440	
	: INFORMATION FOR SEQ ID NO.: 19:	
	: SEQUENCE CHARACTERISTICS:	
	: LENGTH: 490 base pairs	
	: TYPE: nucleic acid	
	: STRANDEDNESS: double	
	: TOPOLOGY: linear	
	: US-09-003-198A-19	
	Query Match 93.6%; Score 234; DB 4; Length 490;	
	Best Local Similarity 100.0%; Pred. No. 3.4e-70;	
	Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
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Dd		
	120 CTCTTTGTGGCACAGAATTTGTGGTGACAGAAGCCAGAATGTGAAGATTGGCAGAT	179
OY	AAATTAGGGAGCCATGCTTGT	188
Dd		
	129 AAATTAGGGAGCCATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	188
Dd		
	180 AAATTAGGGAGCCATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	239

QY 189 GTTAGTGGAAAGGTGTAGGAGCAGCACTCCCGCTGCTGTACTAAAGATGTAA 242  
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Db 240 GTTAGTGGAAAGGTGTAGGAGCAGCACTCCCGCTGCTGTACTAAAGATGTAA 293

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RESULT 5
US-08-766-355-10
: Sequence 10, Application US/08766355
: Patent No. 6121436
:
GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shan, Dilip Maganlal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakim, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 77210
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/766,355
: FILING DATE: Concurrently herewith
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MOBT:063
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 507 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
FEATURE:
: NAME/KEY: modified_base
: LOCATION: one-of(17, 424, 485)
: OTHER INFORMATION: /mod_base= OTHER
: OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-10
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Query Match 93.6%; Score 234; DB 3; Length 507;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 189 GTTATGAGAGGTGTGAGGAGCACTTCCGCTGCTGTGTTACTAAAGATGTTAA 242

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Db 257 GTTACTGGAAGGTGTAAGGACGACTTCGCTGCTGCTGTAATAAAGATGTTAA 310

## RESULT 6

US-09-003-198A-10  
Sequence 10, Application US/09003198A

Patent No. 6316407

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip Maganlal

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Hakiml, Salim

TITLE OF INVENTION: Antifungal polypeptide and Methods for

NUMBER OF SEQUENCES: 19

CONTROLING Plant Pathogenic Fungi

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,198A

FILING DATE: 07-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: modified\_base

LOCATION: one-of(17, 424, 485)

OTHER INFORMATION: /mod\_base= OTHER

OTHER INFORMATION: /note= "N" = A or C or G or T"

US-09-003-198A-10

Query Match 93.6%; Score 234; DB 4; Length 507;

Best Local Similarity 100.0%; Pred. No. 3.4e-70;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 CAATCTAATCAACTATGAGAGAAATCACTAGCTGCTTATGCTTCTCTTCTGTT 68

Db 77 CAATCTAATCAACTATGAGAGAAATCACTAGCTGCTTATGCTTCTCTTCTGTT 136

Qy 69 CTCCTTGTGTCACAGAAATTTGTGTGACAGAACCCAGACATGTGAGAATTTGGCAGAT 128

Db 137 CTCCTTGTGTCACAGAAATTTGTGTGACAGAACCCAGACATGTGAGAATTTGGCAGAT 196

Qy 129 AATATAGGGGACCATGCTTTAGTGTGTGACACTCACTGACCAACCAAGAGACGA 188

Db 197 AATATAGGGGACCATGCTTTAGTGTGTGACACTCACTGACCAACCAAGAGACGA 256

Qy 189 GTTACTGGAAGGTGTAAGGACGACTTCGCTGCTGCTGTAATAAAGATGTTAA 242

Db 257 GTTACTGGAAGGTGTAAGGACGACTTCGCTGCTGCTGTAATAAAGATGTTAA 310

## RESULT 7

US-09-428-805-10

Sequence 10, Application US/09428805

Patent No. 6329504

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip Maganlal

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Hakiml, Salim

TITLE OF INVENTION: Antifungal polypeptide and Methods for

NUMBER OF SEQUENCES: 14

CONTROLING Plant Pathogenic Fungi

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 77210

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/428,805

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/766,355

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: MOBT:063

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: modified\_base

LOCATION: one-of(17, 424, 485)

OTHER INFORMATION: /mod\_base= OTHER

OTHER INFORMATION: /note= "N" = A or C or G or T"

US-09-428-805-10

Query Match 93.6%; Score 234; DB 4; Length 507;

Best Local Similarity 100.0%; Pred. No. 3.4e-70;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 77 CAATCTAATCAACTATGAGAGAAATCACTAGCTGCTTATGCTTCTCTTCTGTT 136

Qy 69 CTCCTTGTGTCACAGAAATTTGTGTGACAGAACCCAGACATGTGAGAATTTGGCAGAT 128

Db 137 CTCCTTGTGTCACAGAAATTTGTGTGACAGAACCCAGACATGTGAGAATTTGGCAGAT 196

Qy 129 AATATAGGGGACCATGCTTTAGTGTGTGACACTCACTGACCAACCAAGAGACGA 188

Db 197 AATATAGGGGACCATGCTTTAGTGTGTGACACTCACTGACCAACCAAGAGACGA 256

Qy 189 GTTACTGGAAGGTGTAAGGACGACTTCGCTGCTGCTGTAATAAAGATGTTAA 242

Db 257 GTTACTGGAAGGTGTAAGGACGACTTCGCTGCTGCTGTAATAAAGATGTTAA 310





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: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/003,198A
: FILING DATE: 07-JAN-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT:193
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713) 787-1400
: TELEFAX: (713) 787-1440
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: 17
: OTHER INFORMATION: /mod_base= OTHER
: OTHER INFORMATION: /note= "N = A or C or G or T"
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: US-09-003-198A-5
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: Query Match 71.9%; Score 179.8; DB 4; Length 200;
: Best Local Similarity 98.9%; Pred. No. 5.9e-52;
: Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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: QY 43 CTGGCTTATGCTTCCTCTCTTCTGTTCTCTTGTGTCACAGAATAATTGGTGACAGAAG 102
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: QY 103 CCAGAACATGTGAGAAATTGGGACGATTAATATAGGGGACCATGCTTTAGTGTGACA 162
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: QY 163 CTCACCTGACAAACCAAGAGACGCGAGTGTAGGAGGTGTAGGAGCGACTTCCGCTGCT 222
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: DB 138 CTCACCTGACAAACCAAGAGACGCGAGTGTAGGAGGTGTAGGAGCGACTTCCGCTGCT 197
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: QY 223 GGT 225
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: DB 198 GCT 200
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: RESULT 11
: US-09-428-805-5
: Sequence 5, Application US/09428805
: Patent No. 6329504
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Maganlal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakiml, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:

```

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: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 77210
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/428,805
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/766,355
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: MOBT:063
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: 17
: OTHER INFORMATION: /mod_base= OTHER
: OTHER INFORMATION: /note= "N = A or C or G or T"
:
: US-09-428-805-5
:
: Query Match 71.9%; Score 179.8; DB 4; Length 200;
: Best Local Similarity 98.9%; Pred. No. 5.9e-52;
: Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
:
: QY 43 CTGGCTTATGCTTCCTCTCTTCTGTTCTCTTGTGTCACAGAATAATTGGTGACAGAAG 102
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: DB 18 CAGGCTTATGCTTCCTCTCTTCTGTTCTCTTGTGTCACAGAATAATTGGTGACAGAAG 77
:
: QY 103 CCAGAACATGTGAGAAATTGGGACGATTAATATAGGGGACCATGCTTTAGTGTGACA 162
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: DB 78 CCAGAACATGTGAGAAATTGGGACGATTAATATAGGGGACCATGCTTTAGTGTGACA 137
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: QY 163 CTCACCTGACAAACCAAGAGACGCGAGTGTAGGAGGTGTAGGAGCGACTTCCGCTGCT 222
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: DB 138 CTCACCTGACAAACCAAGAGACGCGAGTGTAGGAGGTGTAGGAGCGACTTCCGCTGCT 197
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: QY 223 GGT 225
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: DB 198 GCT 200
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: RESULT 12
: US-08-766-355-6
: Sequence 6, Application US/08766355
: Patent No. 6121436
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Maganlal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakiml, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:

```

ADDRESS: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,355  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MOBT:063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: one-of(17, 265)  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = A or C or G or T"  
US-08-766-355-6

Query Match 67.8%; Score 169.6; DB 3; Length 293;  
Best Local Similarity 86.2%; Pred. No. 2.1e-48;  
Matches 187; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
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DB 137 CTCCTTTGTTGACAGAAATTTGGTGACAGAGCCAGACATGTGAGAAATTTGGCAGAT 196  
QY 129 AATATAGGGGACATGCTTTAGTGTGTGACACTGACCTGACCAACCAAGAGAGAGCA 188  
DB 197 ACATACAGGGGACATGCTTCGTTGTTGACTTTCACCTGCAAAACCAAGACACTTA 256  
QY 189 GTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGCT 225  
DB 257 CTTAGCGNAGGTGACAGGAGCAGCTTCGCTGCTGCT 293

RESULT 13  
US-09-003-198A-6  
Sequence 6, Application US/09003198A  
Patent No. 6316407  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakimi, Salim  
TITLE OF INVENTION: Antifungal polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston

STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,198A  
FILING DATE: 07-JAN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT:193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: one-of(17, 265)  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = A or C or G or T"  
US-09-003-198A-6

Query Match 67.8%; Score 169.6; DB 4; Length 293;  
Best Local Similarity 86.2%; Pred. No. 2.1e-48;  
Matches 187; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 9 CAATCTAATCAACATGAGAGAGAAATCAGTGGCTTATGCTTCCTCTTGGT 68  
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QY 129 AATATAGGGGACATGCTTTAGTGTGTGACACTGACCTGACCAACCAAGAGAGCA 188  
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QY 189 GTTAGTGAAGGTGTAGGAGCAGCTCCGCTGCTGCT 225  
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RESULT 14  
US-09-428-805-6  
Sequence 6, Application US/09428805  
Patent No. 6329504  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip Maganlal  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
APPLICANT: Hakimi, Salim  
TITLE OF INVENTION: Antifungal polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 77210  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /note="N = A or C or G or T"
US-09-428-805-6
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Query Match          67.8%: Score 169.6; DB 4; Length 293;
Best Local Similarity 86.2%: Pred. No. 2.1e-48;
Matches 187; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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DB 77 CAATCTAATCAACATATGAGAGAGAATCAGTACGCTTATGCTTCTCTCTCTGTT 136
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QY 69 CTCCTTGTGCACAGAAATTTGTGTGACAGAACGACACATGTGAGAAATTTGGCAGAT 128
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QY 129 AATATAGGGGACATGCTTTAGTGTGACACTCACTGACCAACCAAGAGAGACGA 188
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DB 197 ACATACAGGGGACATGCTTGTGTTGTGACTTCACTGCAAAAACCAAGAGACACTTA 256
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QY 189 GTTACTGAGAGGTGAGGAGCAGCTTCCGCTGCTGCT 225
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DB 257 CTTAGCGGAGAGGTGAGGAGCAGCTTCCGCTGCTGCT 293
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## RESULT 15

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US-08-766-355-9
; Sequence 9, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakiml, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note="N = A or C or G or T"
US-08-766-355-9
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Query Match          47.1%: Score 117.8; DB 3; Length 327;
Best Local Similarity 94.6%: Pred. No. 8.7e-31;
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 114 GAGAAATTTGGCGATTAATATAGGGGACCATCTTTAGTGTGACACTGACGACA 173
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
DB 1 GAGAAATTTGGCGATTAATATAGGGGACCATCTTTAGTGTGACACTGACGACA 60
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
QY 174 ACCAAGAGACGACGTTAGTGAAGGTGAGGAGGACTTCCGCTGCTGTTACTTAA 233
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
DB 61 ACCAAGAGACGACGTTAGTGAAGGTGAGGAGGACTTCCGCTGCTGTTACTTAA 120
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
QY 234 AGATGTTAA 242
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DB 121 AGATGTTAA 129
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Search completed: June 21, 2003, 06:15:19  
Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 05:33:55 ; Search time 107 Seconds  
(without alignments)  
3428.568 Million cell updates/sec

Title: US-10-010-731-13

Perfect score: 250  
Sequence: 1 GGGATTCCTCATCTAATCA.....AAAGATGTTAAGATCCCC 250

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA.\*  
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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	250	9	US-10-010-731-13
2	234	93.6	490	9	US-10-010-731-19
3	234	93.6	507	9	US-10-010-731-10
4	181.2	72.5	189	9	US-10-010-731-18
5	179.8	71.9	200	9	US-10-010-731-5
6	169.6	67.8	293	9	US-10-010-731-6
7	119.4	47.8	494	9	US-09-805-694B-5
8	117.8	47.1	327	9	US-10-010-731-9
9	116.4	46.6	563	9	US-10-178-213-439
10	93.4	37.4	420	9	US-10-178-213-436
11	91.6	36.6	464	9	US-10-178-213-379
12	91.6	36.4	461	9	US-10-178-213-451
13	62	24.8	62	9	US-10-010-731-11
14	48.8	19.5	338	9	US-10-178-213-427
15	47	18.8	47	9	US-10-010-731-12
16	44.2	17.7	438	9	US-10-178-213-418
17	44.2	17.6	455	9	US-10-178-213-415
18	44	17.6	293	9	US-10-178-213-421
19	40	16.0	141	10	US-09-739-384-35

C	20	36	14.4	14485	10	US-09-876-216-3	Sequence 3, Appl1
	21	35.2	14.1	273	10	US-09-878-574-11922	Sequence 11922, A
	22	32.8	13.1	466	9	US-10-178-213-385	Sequence 385, App
	23	31.6	12.6	468	9	US-10-178-213-316	Sequence 316, App
C	24	31.6	12.6	1097	9	US-09-938-842A-4122	Sequence 4122, App
	25	31.4	12.6	2052	12	US-10-007-693-150	Sequence 1150, App
	26	30.8	12.3	1563	10	US-09-731-872-104	Sequence 104, App
	27	30.6	12.2	246	10	US-09-878-574-12979	Sequence 12979, A
	28	30.6	12.2	272	10	US-09-878-574-10791	Sequence 10791, A
	29	30.6	12.2	275	10	US-09-878-574-14296	Sequence 14296, A
	30	30.6	12.2	277	10	US-09-878-574-11794	Sequence 11794, A
C	31	30.6	12.2	361	10	US-09-878-574-1139	Sequence 1139, App
	32	30.6	12.2	502	10	US-09-920-300A-834	Sequence 834, App
C	33	30.6	12.2	502	12	US-10-033-528-834	Sequence 834, App
C	34	30.6	12.2	620	10	US-09-770-149-795	Sequence 795, App
C	35	30.6	12.2	1094	9	US-09-910-664-101	Sequence 101, App
	36	30.6	12.2	3058	9	US-10-106-698-468	Sequence 468, App
	37	30.4	12.2	1083	10	US-09-204-134-1	Sequence 1, Appl1
C	38	30.4	12.2	3791	10	US-09-757-100B-1	Sequence 11517, A
	39	30.2	12.1	463	9	US-09-918-995-11517	Sequence 346, App
C	40	30.2	12.1	609	9	US-10-178-213-346	Sequence 415, App
C	41	30.2	12.1	1036	10	US-09-822-849A-415	Sequence 13620, A
	42	30	12.0	264	10	US-09-878-574-13620	Sequence 319, App
	43	30	12.0	425	9	US-10-178-213-319	Sequence 218, App
	44	30	12.0	1645	9	US-10-102-806-218	Sequence 5117, App
C	45	30	12.0	2000	9	US-09-938-842A-5117	

## ALIGNMENTS

RESULT 1  
US-10-010-731-13  
Sequence 13, Application US/10010731  
Publication No. US20030041347A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip Maganlal  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/010,731  
FILING DATE: 13-No. US20030041347A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/003,198  
FILING DATE: 07-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT:193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1440  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-010-731-13

Query Match 100.0%; Score 250; DB 9; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,1e-74;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGATCCCAATCTATCAACTATGAGAGAGAAATCACTAGCTTATGCTTCTCT 60  
DB 1 GGGGATCCCAATCTATCAACTATGAGAGAGAAATCACTAGCTTATGCTTCTCT 60  
QY 61 TCTTGGTCTCTTTTGGCACAAGAAATGTGTGACAGAACCGAAGCATGTGAGAA 120  
DB 61 TCTTGGTCTCTTTTGGCACAAGAAATGTGTGACAGAACCGAAGCATGTGAGAA 120  
QY 121 TGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGACACTGACACACCAAG 180  
DB 121 TGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGACACTGACACACCAAG 180  
QY 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGACCTCCGCTGCTGTACTAAAGATGTT 240  
DB 181 AGAAGCGAGTTAGTGAAGGTGTAGGAGACCTCCGCTGCTGTACTAAAGATGTT 240  
QY 241 AAGGATCCCC 250  
DB 241 AAGGATCCCC 250

## RESULT 2

US-10-010-731-19  
Sequence 19, Application US/10010731  
Publication No. US20030041347A1

## GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakiml, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-010-731-19

Query Match 93.6%; Score 234; DB 9; Length 490;  
Best Local Similarity 100.0%; Pred. No. 4,1e-69;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAATTAATCAACATATGAGAGAGAAATCACTAGCTTATGCTTCTCTCTTGTG 68  
DB 60 CAATTAATCAACATATGAGAGAGAAATCACTAGCTTATGCTTCTCTCTTGTG 119  
QY 69 CTCCTTGTGACAGAAATGTGTGACAGAACCGAAGCATGTGAGAAATTTGGCAGAT 128  
DB 120 CTCCTTGTGACAGAAATGTGTGACAGAACCGAAGCATGTGAGAAATTTGGCAGAT 179  
QY 129 AATATAGGGGACCATGCTTTAGTGTGTGACACTGACACCAAGCAAGACCA 188  
DB 180 AATATAGGGGACCATGCTTTAGTGTGTGACACTGACACCAAGCAAGACCA 239  
QY 189 GTTACTGGAAGGTGTAGGAGACCTCCGCTGCTGTACTAAAGATGTTAA 242  
DB 240 GTTACTGGAAGGTGTAGGAGACCTCCGCTGCTGTACTAAAGATGTTAA 293

## RESULT 3

US-10-010-731-10  
Sequence 10, Application US/10010731  
Publication No. US20030041347A1

## GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakiml, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

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: NAME/KEY: modified base
: LOCATION: one-of(17, 424, 485)
: OTHER INFORMATION: /mod_base= OTHER
: /note= "N = A or C or G or T"
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: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-731-10

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Query Match 93.6%; Score 234; DB 9; Length 507;  
Best Local Similarity 100.0%; Pred. No. 4.2e-69;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
77 CAATCTATCAAACTATGAGAAACAATCACTAGCTGGCTTATGCTTCCTCTTCGTT 136  
Db

QY 69 CTTCTTGTGTGCACAGAATTTGTGTGACAGAACCCAGACATGTGTGAATTTGGCGAT 128  
 |||||  
 Db 137 CTTTGTGTGCACAGAATTTGTGTGACAGAACCCAGACATGTGTGAATTTGGCGAT 196

Dy 129 AATATATAGGGGACCATTGCCTTTAGTGGTTGTGACACTCAGTCACCAACAAGAAGACGCA 188  
|||  
Db 197 AATATATAGGGGACCATTGCCTTTAGTGGTTGTGACACTCAGTCACCAACAAGAAGACGCA 256

Qy 189 GTTAGTGGAGGCTGTAGGACACTTCCGCTGCTGTACTAATAAGATGTTAA 242  
 |||||  
 Db 257 GTTAGTGGAGGCTGTAGGACACTTCCGCTGCTGTACTAATAAGATGTTAA 310

RESULT 4  
US-10-010-731-18  
Source 18  
Investigation no. 00010771

Publication NO. US20030041347A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip Vasantlal

Wu, Yonnie S.  
 Rosenberger, Cindy A.  
 Hakim, Salim  
 TITLE OF INVENTION: Artificially Polysaccharide and Water-Imm

Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: Arnold White & Davies

STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA

```

;
;      ZIP: 77210
;
;      COMPUTER READABLE FORM:
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;      MEDIUM TYPE: Floppy disk
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;      COMMENTS: IBM PC (model 486)

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;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: 05/10,010 733
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FLILING DATE: 13-NO. US20030041347A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 00/003 109

FILING DATE: 07-JAN-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Patterson, Melinda L.  
 REGISTRATION NUMBER: 33 063

REFERENCE/DOCKET NUMBER: MOB1-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
TELEFAX: (713) 787-1400

```

;
; INFORMATION FOR SEQ ID NO: 18:
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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 189 base pairs
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; TYPE: nucleic acid
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STRANDEDNESS: double
TOPOLOGY: linear
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SEQUENCE	DESCRIPTION:	SEQ	ID NO:	18:
US-10-010-731-18				

Query Match	72.5%;	Score 181.2;	DB 9;	Length 189;
Best Local Similarity	98.4%;	Pred. No. 2e-51;		
Matches 183; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

**Dy** 43 CTGGGCTATGCCTTCCTCTTGTGTTCTCTTGTGCACAAAGAAATTGTGTGACAGAAC 102  
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**Db** 1 CAGGCTTATGCTCCCTCTTCTTGSTGTTCTCTTGTGCACAAGAAATTGTGTGACAGAAC 60

QY 103 CCAGAACATGTGAGAAATTTGGCGAGATAATATATGGGGAGCCATCGTTTGTGCTGTGACA 162  
D6 61 CCAGAACATGTGAGAAATTTGGCGAGATAATATATGGGGAGCCATCGTTTGTGCTGTGACA 120

QY 163 CTCACATGCACACCAAGAGAGAACGACAGTTAGTGGAAAGGTAGGAGACACTTCCGCTCGT 222

Dδ 121 CTCACATGCACACCAAGAGAGAACGACAGTTAGTGGAAAGGTAGGAGACACTTCCGCTCGT 180

QY	223	GGTGA	228
Db	181	GCTGA	186

RESULT 5  
US-10-010-731-5

PublicationNO. US20030041347A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong

Wu, Yonnie S.  
Rosenberger, Cindy A.  
Hakimi, Salim

Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES : 19  
CORRESPONDENCE ADDRESS:

STREET: P.O. Box 4433  
City: Houston  
STATE: Texas  
COUNTRY:

```

:
:
:      ZIP: 77210
:      COMPUTER READABLE FORM:
:      MEDIUM TYPE: Floppy disk
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;      .
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: Patentin Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA: ... ..

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3  : FILING DATE: 13-NO. US20030041347A1-2001
4  : CLASSIFICATION: <Unknown>
5  : PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: MOBT:193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 787-1400  
MORRIS, JAMES J.

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 200 base pairs
;     molwt: 66000
;

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```

;
; STRANDEDNESS: double
; TOPOLOGY: linear
FEATURE:
NAME/key: modified base

```

```

; LOCATION: 17
; OTHER INFORMATION: /mod_base= OTHER

```







```
APPLICANT: Navaro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 436
LENGTH: 420
TYPE: DNA
ORGANISM: Cyamopsis tetragonoloba
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(264)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (116)...(261)
US-10-178-213-436
```

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Query Match      37.4%: Score 93.4; DB 9; Length 420;
Best Local Similarity 69.7%: Pred. No. 1.7e-21;
Matches 175; Conservative 0; Mismatches 61; Indels 15; Gaps 3;
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```
OY 14 TAAATCAACTATGAGGAAGAATCACTAGCTGCTTATGCTTCCCTC---TTCTTGCTTCT 70
DB 21 TAAAGTAATTTATGAGAGAGAAATCACTGCTGATTTGGTCCCTCATCTCTGTTGTTGT 80
OY 71 CTCTTGTCACAAAGAAATTTGTGTG---ACAGAACCCAGAACATGTGAAATTTGCGAGA 127
DB 81 GTTACTTGGCAGAGAAAGTAGTGTGTAACAAACAGAGGAAAGACATGTGAAATCTTGCGA 140
OY 128 TAAATATAGGGGACCATCTTATGTG-----GTTGTGACACTCACTGCACAACCA 178
DB 141 TACATTCAGGGGTCTTCCTCCCTGGAACCCGACAGTCACATGTCAGAACAA 200
OY 179 AGAGAACCCAGTTAGTGAAGGTGAGGAGACATTCGCTGCTGTGTAATAAAGATG 238
DB 201 AGAGCACTTGTCTACAGCGAAGGTGACAGACGATTTTCTGCTGTCACCAAAAACGTG 260
OY 239 TTAAGGATCCC 249
DB 261 TTAATTCCCCC 271
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RESULT 11
US-10-178-213-379
; Sequence 379, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navaro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
```

```
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 379
LENGTH: 464
TYPE: DNA
ORGANISM: Cyamopsis tetragonoloba
FEATURE:
NAME/KEY: CDS
LOCATION: (32)...(256)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (116)...(253)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379
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Query Match      36.6%: Score 91.6; DB 9; Length 464;
Best Local Similarity 71.6%: Pred. No. 7.2e-21;
Matches 166; Conservative 0; Mismatches 54; Indels 12; Gaps 3;
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OY 20 AACTATGAGAGAAGAAATCACTAGCTGCTTATGCTTCCCTTCTGTTCTTCTTGTGC 79
DB 28 AATTATGAGAGAAGAAATCACTAGCTGCTGTTTGTGCTCTCTCTCTCTCTTGTGCTGC 87
OY 80 ACAAGAAATTTGTGTG---ACAGAACCCAGAACATGTGAGAAATTTGGCAGATTAATATAG 136
DB 88 TCAGAAATATAGTGTGGAAGAACAGAGCAAGAACATGTGAGAGTCCGCGACACATACAG 147
OY 137 GGGACCATGCTTAA-----GTGTTGTGACACTACAGCACAACCAAGAACGCGACT 190
DB 148 GGGACCTGTTTCACTAGGAGGTGATGCTGCTGATGATCATTTGCAAGAACCAACTTAA 207
OY 191 TAGTGAAGGTGTAGGAGACGACTTCGCTGCTGTTGTAATAAAGATGTTAA 242
DB 208 CAGTGAACATGCA---AACAGTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
```

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RESULT 12
US-10-178-213-451
; Sequence 451, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navaro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 451
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Atachis hypogaea
; FEATURE:
; NAME/KEY: CDS
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DB 200 TGCCGAGCTTCCGCCGTGCTGT 223

## RESULT 15

US-10-010-731-12/C

; Sequence 12, Application US/10010731

; Publication No. US20030041347A1

; GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Nu, Yontie S. Cindy A.

Rosenberger, Cindy A.

Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-NO. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MORT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-010-731-12

Query Match 18.8%; Score 47; DB 9; length 47;

Best Local Similarity 100.0%; Pred. NO. 2.9e-06;

Matches 47; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

DB 204 AGGAGCACTTCCGCTGCTGTAAGATGTAAGATCCCC 250

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Search completed: June 21, 2003, 06:17:16

Job time : 109 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 03:56:28 ; Search time 1132 Seconds  
(without alignments)  
3576.742 Million cell updates/sec

Title: US-10-010-731-13  
Perfect score: 250  
Sequence: 1 GGGGATCCCAATCTAATCA.....AAAAGATGTTAGAGATCCC 250

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184.6	73.8	446	9 AJ498901	AJ498901 AJ498901
2	118.2	47.3	574	14 B0151477	B0151477 NF088A06L
3	118	47.2	517	9 AJ308155	AJ308155 AJ308155
4	116.2	46.3	487	13 BI321179	BI321179 saF48d10.
5	114.6	45.8	426	12 BG838678	BG838678 GC01_03f0
6	102.8	41.1	503	12 BF633403	BF633403 NF047E03D

7	87.6	35.0	438	13 BI642738	BI642738 TS21161 T
8	61.4	24.6	238	13 BI642792	BI642792 TS21220 T
9	49	19.6	366	9 AJ503961	AJ503961 AJ503961
10	49	19.6	366	13 BI321308	BI321308 saF50C11.
11	49	19.6	447	13 BI269947	BI269947 NF01/G121
12	49	19.6	452	12 BG450155	BG450155 NF014H03D
13	49	19.6	452	12 BG452703	BG452703 NF079E01L
14	49	19.6	466	14 B0157500	B0157500 NF105E081
15	47	18.8	543	12 BG453394	BG453394 NF090E11L
16	43.8	17.5	372	9 AJ498451	AJ498451 AJ498451
17	42.8	17.1	319	9 AJ375191	AJ375191 MEB11H12
18	42	16.8	550	9 AJ373581	AJ373581 MEBB01F04
19	41.8	16.7	203	9 AJ379949	AJ379949 MEBB48D07
20	41.8	16.7	354	9 AJ376623	AJ376623 MEBB25A10
21	41.8	16.7	383	9 AJ379948	AJ379948 MEBB48D07
22	41.8	16.7	432	9 AJ377785	AJ377785 MEBB33H07
23	41.8	16.7	436	9 AJ378977	AJ378977 MEBB41F04
24	41.8	16.7	440	9 AJ380895	AJ380895 MEBB55C03
25	41.8	16.7	443	9 AJ375904	AJ375904 MEBB19H02
26	41.8	16.7	445	9 AJ375903	AJ375903 MEBB19H02
27	41.8	16.7	450	9 AJ377784	AJ377784 MEBB33H07
28	41.8	16.7	456	9 AJ377705	AJ377705 MEBB33C10
29	41.8	16.7	459	9 AJ377706	AJ377706 MEBB33C10
30	41.8	16.7	461	9 AJ380896	AJ380896 MEBB55C03
31	41.8	16.7	473	9 AJ373658	AJ373658 MEBB02A12
32	41.8	16.7	479	9 AJ375897	AJ375897 MEBB19G10
33	41.8	16.7	483	9 AJ380879	AJ380879 MEBB55B05
34	41.8	16.7	490	9 AJ376002	AJ376002 MEBB20F02
35	41.8	16.7	491	9 AJ374748	AJ374748 MEBB09A01
36	41.8	16.7	534	10 AW980646	AW980646 EST391799
37	41.8	16.7	552	9 AJ374749	AJ374749 MEBB09A01
38	41.8	16.7	701	14 B0255321	B0255321 MTNNAK6TFK
39	40.2	16.1	418	9 AJ377999	AJ377999 MEBB35C11
40	40.2	16.1	494	9 AJ373580	AJ373580 MEBB01F04
41	39.4	15.8	331	12 BG453276	BG453276 NF088B09L
42	39.4	15.4	475	13 BI269021	BI269021 NF016B051
43	38.6	15.4	364	9 AJ498976	AJ498976 AJ498976
44	38.6	15.4	452	12 BG451938	BG451938 NF043B11D
45	38	15.2	454	12 BG451992	BG451992 NF043B03D

## ALIGNMENTS

RESULT 1  
AJ498901  
LOCUS  
DEFINITION  
AJ498901 MTP0SE Medicago truncatula cDNA clone mt-acc955209h10,  
mRNA sequence.  
ACCESSION  
AJ498901  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
barrel medic.  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.  
1 (bases 1 to 446)  
Firnhaber,C., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T.,  
Linke,B., Puehler,A. and Kuester,H.  
Determination of transcript sequences from developing pods  
including seeds of Medicago truncatula genotype Al7  
Unpublished (2002)  
Contact: Kuester H  
Lehrstuhl fuer Genetik  
Universitaet Bielefeld  
Postfach 100131, D-33501 Bielefeld, Germany.  
Location/Qualifiers  
1..446  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="mt-acc955209h10"

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	202; Conservative	73.8%; Score 184.6; DB 9; Length 446; 87.4%; Pred. No. 2.7e-47; Mismatches 29; Indels 0; Gaps 0;
147 a	84 c	83 g	132 t			
<p>/clone.lib="MTP0SF"            /tissue_type="pods including seeds"            /dev_stage="different stages of development"            /note="Vector: pGEM-T; Site_1: PstI; Site_2: SphI;            genotype A17; cDNA was prepared from polyA+ enriched RNA            from developing pods including seeds harvested at            different stages of development. The cDNA was            directionally ligated by Medigenomix into the pGEM-T            vector from Promega using CGATCGCCGACGCGCCGACATG and            CTCGAGGCCATTATGCGCGG adapters. Plasmids containing cDNA            inserts were propagated in E. coli DH10B cells."</p>						
Oy	12	TCATATCAATATGAGAGAAATCTACTAGCTGGCTTATGCTTCCTTCCTGGTCTC	71			
Db	49	TATCACTAAGCTATGAGAGAAAACTACAGAGCTTATGCTTCCTTCCTGGTCTC	108			
Oy	72	TTTGTTGACAGAAATGTGTGTACAGAACCCAGACATGTGAAATTTGGCAGATAA	131			
Db	109	TTTGTTGACAGAAATGTGTGTACAGAACCTTAAGACTTGTGAAATTTGGCAGATAA	168			
Oy	132	TATAGGAGCAGCTGTTAGTGTGTGTGACACTCAGTCAACCAAGAAAGACAGT	191			
Db	169	TACAGGGAGCATGTTAGTGTGTGTGATACTCAGTCACTACCAAGAAATGCACTT	228			
Oy	192	AGTGAAGGTATGAGGACGACTTCGCGTGTGTGTACTAAAGATGTAA	242			
Db	229	AGCGCAGCTCAGGAGATGACTTTCGTTGTGTGTACTAAAACTGTAA	279			
RESULT 2						
LOCUS	B0151477	574 bp	mRNA	linear	EST 24-APR-2002	
DEFINITION	NF088A06LF1038	Developing leaf	Medicago truncatula	CDNA clone		
ACCESSION	B0151477					
VERSION	B0151477.1	GI:20288536				
KEYWORDS	EST.					
SOURCE	barrel medic.					
ORGANISM	Medicago truncatula					
REFERENCE	Medicago truncatula					
AUTHORS	Eunatryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
TITLE	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
JOURNAL	Rosidae; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;					
COMMENT	Medicago.					
	1 (bases 1 to 574)					
	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,					
	Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.					
	Expressed Sequence Tags from the Samuel Roberts Noble Foundation					
	Medicago truncatula leaf library					
	Unpublished (2000)					
	Contact: May GD					
	Plant Biology Division					
	The Samuel Roberts Noble Foundation					
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA					
	Tel: 580 221 7391					
	Fax: 580 221 7380					
	Email: gdmay@noble.org					
	Insert Length: 574	Std Error: 0.00				
	Plate: 088	row: A	column: 06			
	Seq primer: TCACACAGAAACAGCATATGAC.					
FEATURES	Location/Qualifiers					
SOURCE	1..574					
	/organism="Medicago truncatula"					
	/db_xref="taxon:3880"					
	/clone="NF088A06LF"					
	/clone.lib="developing leaf"					
	/tissue_type="leaf"					
	/dev_stage="pooled developmental"					

		/note="vector: Lambda zap; Contains a mixture of very young, developing, mature and senescing leaves."
BASE COUNT	198 a	104 c
ORIGIN	167 t	1 others
Query Match	47.3%	Score 118.2; DB 14; Length 574;
Best Local Similarity	74.3%;	Pred. No. 2.6e-26;
Matches 179;	Conservative	0; Mismatches 53; Indels 9; Gaps 2.
OY	9 CAATCTAATCAACATGAGAGAAGAAATCAGTGGCTGTATGCCTTCCTTTGGTT  Db 44 CACATATCTTTAAGCGATGAGAGACAATAATAGTGGCTTGCTTACTTCTCCSTT   OY 69 CTCCTTTGTTGCCAACAGAAATTGTGTGCAGAGACCAGACATGTGAAATTTGGCAGAT   Db 104 CTCCTTTGTTGCCAACAGAAATTGCGGTGACTGAACGAGACTTGTGACCATTTGGCTGAT   OY 129 AATAATAGGGAGCACATGCTTTA-----GTGGTTGTGCACTCACTGACACCAACCAAGAG   Db 164 ACATATACAGAGGACCATGCTTACGGAAAGGTAGCTGTGATGACCACTGCAAMAAACGA   OY 183 AACCCAGTTAATGGAAGGTGTAAGGACACACTTCGCTCTCTGTGTACTAAAAAGATGTAA   Db 224 CACCTTAATTAATGGCAGCT---GCCATAACTTTCAATGTCTTCTGCACCTCAAACACTTTAA   OY 243 C 243   Db 281 G 281	

[illegible]

FEATURES	SOURCE
<p>RESULT 4</p> <p>B1321179</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ACCESSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>JOURNAL</p> <p>COMMENT</p>	<p>487 bp mRNA linear EST 29-NOV-2001</p> <p>sat48d10.y3 Gm-cl077 glycine max cdna clone GENOME SYSTEMS CLONE</p> <p>ID: Gm-cl077-1723 5' similar to SW:10KD_VICUN P18646.10 KD PROTEIN</p> <p>PRECUSOR ;, mRNA sequence.</p> <p>B1321179</p> <p>B1321179.1 GI:15000365</p> <p>EST.</p> <p>soybean.</p> <p>Glycine max</p> <p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.</p> <p>1 (bases 1 to 487)</p> <p>Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, D., Beck, C., Wylie, F., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.</p> <p>Public Soybean EST Project</p> <p>unpublished (1999)</p> <p>Contact: Shoemaker R/Public Soybean EST Project</p> <p>Public Soybean EST Project</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: est@wustl.wustl.edu</p> <p>Putative full length read</p> <p>vector to vector length is this clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801</p> <p>For further information call: (800)-533-4363 or contact via email: c@resgen.com</p> <p>Seq primer: -40RP from Gldco</p> <p>High quality sequence stop: 432.</p> <p>Location/Qualifiers</p> <p>1..487</p> <p>/organism="Glycine max"</p> <p>/db_xref="taxon:3847"</p> <p>/clone="GENOME SYSTEMS CLONE ID: Gm-cl077-1723"</p> <p>/clone_1id="Gm-cl077"</p> <p>/tissue-type="18 day old 'Williams' seedlings"</p> <p>/dev_stage="18 day old 'Williams' seedlings"</p> <p>/lab_host="DH10P"</p> <p>/note="Vector: pluescript II SK+; site_1: EcoRI; site_2: XhoI; The mRNA was isolated from cotyledons of 18-day-old 'Williams' seedlings which were greenhouse grown in potting soil. The cotyledons were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number. 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer [GACAGACAGACAGACAGACAGACTAGCTGTGAC(T)188V to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled.</p>

in with cloned *Pfu* DNA, ligated to *ECORI* adaptors and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The *XhoI* site within the first-strand synthesis primer was then restricted by digestion with *XhoI* from Promega (400U/ul); all *XhoI* sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II, XR predigested vector (pBluescript II SK(+)) vector that has been digested with *ECORI* and *XhoI*, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Corryell at Northern Arizona University."

Query Match	Best Local Similarity	46.5%;	Score 116.2;	DB 13;	Length 487;
Matches	177;	Conservative	0;	Mismatches 53;	Indels 9;
					Gaps 2;
QY	13	CTAATCAACATATGAGAGAAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTGGTGTCT	72		
Db	57	CTAATTAAGCATGATGAGAGAAATCAATAGCTGGGTTGTGCTTCCTCTTCTTCTCT	116		
QY	73	TTGTTGCACAAAGAATTTGTGTG---ACAGAGCCAGACATGTGAGATTTGGCAGATA	129		
Db	117	TTGTTGCTCAAGAAAGTTGTGTGTGCAAACTGAGGGAAGACTTGGAGAACTGGCTGATA	176		
QY	130	AATTTAGGGGACCATTCCTT-----TATGTGTTTGACACTCACTGACCAACAAAGAGA	183		
Db	177	CATACAGAGGGCTCATCTGCTTACACACTGGCAGCTCGATTTTTCGACAGACAAAGAGC	236		
QY	184	ACGCAGTTAGTGAAGGTGTAGGAGCAGACTTCGCTGCTGTACTAAAGATGTTAA	242		
Db	237	ACTTGCTCAGAGCAGATGCAGGAGCAGATTTTTCCTGTTGGTGCACCAAAACGTGTAA	295		
RESULT 5	BG838678/c	426 bp	mrna	linear	EST 25-MAY-2001
LOCUS	BG838678	GC01_03f01.A	GAFC.EOCR	cold stressed	Glycine_clandestina
DEFINITION	Glycine_clandestina cDNA clone GC01_03f01, mRNA sequence.				
ACCESSION	BG838678				
VERSION	BG838678.1	GI:14204985			
KEYWORDS	EST.				
SOURCE	Glycine_clandestina				
ORGANISM	Glycine_clandestina				
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.				
REFERENCE	1 (bases 1 to 426)				
AUTHORS	Singh,J.A., Farrah,S., Chapados,J., Couroux,P., De Moors,A., Harris ,L.J., Hattori,J.I., Ouellet,T., Koberl,L.S., Sprott,D. and Tinker ,N.A.				
TITLE	Expressed Sequence Tags from Cold-Stressed Glycine_clandestina Seedlings				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Singh,J.A. Oilseed Research Centre Eastern Cereal and Agri-Food Canada Agriculture and Agri-Food Canada KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0G6, Canada				
FEATURES	tel: (613) 759-1662				
	fax: (613) 759-1701				
	Email: singhja@em.agr.ca.				
	Location/Qualifiers				
source	1. 426				
	/organism="Glycine_clandestina"				

/cultivar="1035"  
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/clone\_1lb="GC01\_AAF01\_EC0RC\_cold\_stressed\_Glycine\_clandest  
ina"  
/tissue\_type="Leaves, stem"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site\_1: EcoRI;  
Site\_2: XhoI; Plants incubated at 2 degrees under 12 hours  
of light/day. Harvested after only 2-3 days of cold  
treatment. cDNA was prepared with the Uni-Zap cDNA kit  
from StrataGene. Eco RI adapters were linked followed by  
digest with Xho I/Eco RI and ligated to pBluescript."  
BASE COUNT 116 a 92 c 86 g 125 t 7 others  
ORIGIN  
Query Match 45.8%; Score 114.6; DB 12; Length 426;  
Best Local Similarity 70.7%; Pred. No. 3.2e-25;  
Matches 176; Conservative 6; Mismatches 58; Indels 9; Gaps 2;  
QY 11 ATCTAATCAACTATGAGAGAGAAATCAGTACTGCTGCTTATGCTTCTCTTGGTCT 70  
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416 ATATCACTAGGCATGAGAGAAATCAGTACTGCTGCTTATGCTTCTCTTGGTCT 357  
416 ATATCACTAGGCATGAGAGAAATCAGTACTGCTGCTTATGCTTCTCTTGGTCT 357  
QY 71 CTTTGTGACAGAAATTTGTGTC--ACAGAGCCAGAACATGTGAGATTGGCAGA 127  
71 CTTTGTGACAGAAATTTGTGTC--ACAGAGCCAGAACATGTGAGATTGGCAGA 127  
356 CTTTGTGACAGAAATTTGTGTC--ACAGAGCCAGAACATGTGAGATTGGCAGA 297  
356 CTTTGTGACAGAAATTTGTGTC--ACAGAGCCAGAACATGTGAGATTGGCAGA 297  
QY 128 TAAATATAGGAGACATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 181  
128 TAAATATAGGAGACATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 181  
296 TACATACAGAGGATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 237  
296 TACATACAGAGGATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 237  
Db 182 GAACGAGTTAGTGAAGGTGAGGAGACACTCCGCTGCTGCTACTAAAGATGTTA 241  
182 GAACGAGTTAGTGAAGGTGAGGAGACACTCCGCTGCTGCTACTAAAGATGTTA 241  
236 ACACCTACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 177  
236 ACACCTACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 177  
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242 AGGATCCCC 250  
Db 176 ATTAAGMCS 168  
176 ATTAAGMCS 168  
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BF633403  
LOCUS NF047E03DT1F1022 Drought Medicago truncatula cDNA clone NF047E03DT  
DEFINITION 5', mRNA sequence.  
ACCESSION BF633403  
VERSION BF633403.1 GI:11897561  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 503)  
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula drought library  
Unpublished (2000)  
JOURNAL  
COMMENT Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org  
Insert Length: 503 Std Error: 0.00  
Plate: 047 row: E column: 03  
Seq primer: TCACACAGGAAACAGCTATGAC.  
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/clone\_1lb="Drought"  
/tissue\_type="Plantlets"  
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/note="Vector: Lambda Zap; Contains a mixture of entire  
plantlets harvested in a series of days-post-watering  
timepoints."  
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Matches 176; Conservative 0; Mismatches 57; Indels 9; Gaps 3;  
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49 CACTATCAATTAAGCGATGAGAGAAATCAGTACTGCTGCTTATGCTTCTCTTGGT 108  
49 CACTATCAATTAAGCGATGAGAGAAATCAGTACTGCTGCTTATGCTTCTCTTGGT 108  
QY 68 TCTCTTTGTCACAGAAATTTGTGTCAGAGAGCCAGAACATGTGAGATTGGCAGA 127  
68 TCTCTTTGTCACAGAAATTTGTGTCAGAGAGCCAGAACATGTGAGATTGGCAGA 127  
109 TCTCTTTGTCACAGAAATTTGTGTCAGAGAGCCAGAACATGTGAGATTGGCAGA 168  
109 TCTCTTTGTCACAGAAATTTGTGTCAGAGAGCCAGAACATGTGAGATTGGCAGA 168  
QY 128 TAAATATAGGAGACATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 181  
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169 TACATACAGAGGATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 228  
169 TACATACAGAGGATGCTTAA-----GTGGTTGACACTGACAGCAACCAAG 228  
QY 182 GAACGAGTTAGTGAAGGTGAGGAGACACTCCGCTGCTGCTACTAAAGATGTTA 241  
182 GAACGAGTTAGTGAAGGTGAGGAGACACTCCGCTGCTGCTACTAAAGATGTTA 241  
229 ACACCTAATTAAGTGGA--CCGTCACATTAATTTCTGACACTCAAAACTGTTA 286  
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Db 287 AG 288  
287 AG 288  
RESULT 7 438 bp mRNA linear EST 10-SEP-2001  
B1642738  
LOCUS T2S1161 TZS (Sapwood-heartwood transition zone of black locust -  
Summer) Robinia pseudocacia cDNA, mRNA sequence.  
ACCESSION B1642738  
VERSION B1642738.1 GI:15544948  
KEYWORDS EST.  
SOURCE Robinia pseudocacia.  
ORGANISM Robinia pseudocacia.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Robinia;  
Robinia.  
1 (bases 1 to 438)  
Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F.,  
Kandem, D.P. and Keathley, D.E.  
Analysis of gene expression patterns in trunk wood of a mature  
black locust (Robinia pseudocacia)  
Unpublished (2002)  
JOURNAL  
COMMENT Contact: Kyung-Hwan Han  
Department of Forestry  
Michigan State University  
126 Natural Resources, East Lansing, MI 48824-1222, USA  
Tel: 517 353 4751  
Fax: 517 432 1143  
Email: hanky@msu.edu.  
FEATURES  
source 1.438  
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/db\_xref="taxon:35938"  
/clone\_1lb="TZS (Sapwood-heartwood transition zone of  
black locust - Summer)"  
/tissue\_type="sapwood-heartwood transition zone"  
/dev\_stage="mature tree"  
/note="Vector: Lambda Triplex; Site\_1: Sfi IA; Site\_2: Sfi  
IB; The cDNA library was made from the sapwood-heartwood





ID: Gm-c1077-2037 5' similar to SW:10KD\_VIGUN P18646 10 KD PROTEIN  
 PRECURSOR ; mRNA sequence.  
 BI321308  
 BI321308.1 GI:15000494  
 EST.  
 SOURCE  
 ORGANISM  
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 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 366)  
 Shoemaker,R., Keim,P., Vodkin,L., Erpeliding,J., Corryell,V., Khanna  
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
 R., Rlter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccann  
 R., Waterston,R. and Wilson,R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: Resgen, Invitrogen Corp, 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact via email: ccut@resgen.com  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 343.  
 Location/Qualifiers  
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 /db\_xref="taxon:3847"  
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 /dev\_stage="18 day old 'Williams' seedlings"  
 /lab\_host="DH10B"  
 /note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2:  
 XhoI; The mRNA was isolated from cotyledons of 18-day-old  
 'Williams' seedlings which were greenhouse grown in  
 potting soil. The cotyledons were flash-frozen in liquid  
 nitrogen. StrataGene's cDNA Synthesis Kit (catalog number  
 200401) was used to synthesize the cDNA. First-strand  
 synthesis was performed with 5-methyl dCTP, hence the  
 ligated cDNA was hemimethylated. A modification of  
 StrataGene's first-strand synthesis primer was used. An  
 'anchor' nucleotide (V-A, C, or G) was added to the 3' end  
 of the primer (GAGAGAGAGAGAGAGAGACTGCTCGAG(T)18V) to  
 anchor the primer at the 5' end of the poly(A) tract.  
 After second-strand synthesis, the cDNA ends were filled  
 in with cloned Pfu DNA, ligated to EcoRI adapters and  
 subsequently phosphorylated. The cDNA was then  
 precipitated and redissolved in sterile, RNase-,  
 DNase-free water. The XhoI site within the first-strand  
 synthesis primer was then restricted by digestion with  
 XhoI from Promega (400/ul); all XhoI sites in the cDNA  
 would be protected by their hemimethylated status. The  
 cDNA constructs were size-fractionated with a 500bp  
 cutoff, using Sephacryl S-500 High Resolution (Pharmacia  
 Biotech) in a 2-mm diameter column and a bed volume of  
 approximately 1ml. The column eluent was precipitated,  
 redissolved, and ligated into StrataGene's pBluescript II  
 XR Predigested vector (pBluescript II SK(+)) vector that  
 has been digested with EcoRI and XhoI, and phosphorylated  
 by StrataGene). This library was constructed in the  
 laboratory of Dr. Paul Keim and Dr. Virginia H. Corryell at  
 Northern Arizona University."

BASE COUNT  
 ORIGIN

124 a 60 c 70 g 112 t

Query Match 19.6%; Score 49; DB 13; Length 366;  
 Best Local Similarity 71.9%; Pred. No. 0.00015;  
 Matches 64; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
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 Db 3 GCGCATGATCATCTCAAGAACAAAGACACTTGTCTCAGAGCAGATCAGGACGATT 62  
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 Oy 214 TCCGCTGCTGCTGCTACTAAAGATGTTAA 242  
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 Db 63 TTGCGTGTGTGTCACCAAAACTGTTAA 91  
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 ACCESSION  
 BI269947  
 VERSION  
 BI269947.1 GI:14877082  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 barrel medic.  
 Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; euroids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 447)  
 Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula irradiated library  
 Unpublished (2001)  
 Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
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 /dev\_stage="seedling"  
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 to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.  
 Gamma-irradiated samples were harvested at 6, 12, 24 and  
 48 hours after treatment. UV-treatment samples were  
 harvested 24 hours post-treatment. cDNA was prepared from  
 polyA+ enriched, pooled samples of equivalent amounts of  
 total RNA from each sample. The cDNA was directionally  
 ligated into the Uni-Zap XR vector (StrataGene) and  
 packaged using the GigaPack III Gold packaging extracts.  
 Plasmids containing cDNA inserts were in vivo excised  
 from the recombinant Uni-Zap XR vector using ExSist  
 helper phage and the E. coli strain XL1-blue MRP'  
 (StrataGene). Excised plasmids were plated using SOLR  
 cells."

FEATURES  
 source

BASE COUNT 157 a 60 c 89 g 141 t  
 ORIGIN

Query Match 19.6%; Score 49; DB 13; Length 447;  
 Best Local Similarity 75.3%; Pred. No. 0.00016;  
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 15 AATCAACTATGAGAAATACACTAGCTGCTTATGCTTCTCTTCTGTTCTTT 74  
 Db 11 AAGAGAGTATGAGAAACACTGCTAGCTGTGCTTCTTCTCATTTGTTCTCTTA 70  
 OY 75 GTTGACACAGAAATTTGTGTG 95  
 Db 71 GCTGCTCAAGACAGCAGTGTG 91

RESULT 12  
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 5', mRNA sequence.  
 ACCESSION BG450155  
 VERSION BG450155.1 GI:13368937  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.  
 1 (bases 1 to 450)  
 REFERENCE Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula drought library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
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 Seq primer: TCACACAGAAACAGCTATGAC.  
 Location/Qualifiers  
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 /dev\_stage="Pooled timepoints"  
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 plantlets harvested in a series of days-post-watering  
 timepoints."  
 BASE COUNT 158 a 60 c 89 g 143 t  
 ORIGIN

Query Match 19.6% Score 49; DB 12; Length 450;  
 Best Local Similarity 75.3%; Pred. No. 0.00016;  
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 15 AATCAACTATGAGAAATACACTAGCTGCTTATGCTTCTCTTCTGTTCTTT 74  
 Db 12 AAGAGAGTATGAGAAACACTGCTAGCTGTGCTTCTTCTCATTTGTTCTCTTA 71  
 OY 75 GTTGACACAGAAATTTGTGTG 95  
 Db 72 GCTGCTCAAGACAGCAGTGTG 92

RESULT 13  
 BG452703  
 LOCUS  
 DEFINITION NF079E01LF1003 Developing Leaf Medicago truncatula cDNA clone  
 452 bp mRNA linear EST 16-MAR-2001  
 ACCESSION BG452703  
 VERSION BG452703.1 GI:13371497

KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.  
 1 (bases 1 to 452)  
 REFERENCE Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 452 Std Error: 0.00  
 Plate: 079 row: E column: 01  
 Seq primer: TCACACAGAAACAGCTATGAC.  
 Location/Qualifiers  
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 /db\_xref="taxon:3880"  
 /clone="NF079E01LF"  
 /clone\_lib="Developing leaf"  
 /tissue\_type="leaf"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: Lambda Zap; Contains a mixture of very  
 young, developing, mature and senescing leaves."  
 BASE COUNT 158 a 60 c 89 g 145 t  
 ORIGIN

Query Match 19.6% Score 49; DB 12; Length 452;  
 Best Local Similarity 75.3%; Pred. No. 0.00016;  
 Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 15 AATCAACTATGAGAAATACACTAGCTGCTTATGCTTCTCTTCTGTTCTTT 74  
 Db 16 AAGAGAGTATGAGAAACACTGCTAGCTGTGCTTCTTCTCATTTGTTCTCTTA 75  
 OY 75 GTTGACACAGAAATTTGTGTG 95  
 Db 76 GCTGCTCAAGACAGCAGTGTG 96

RESULT 14  
 B0157500  
 LOCUS  
 DEFINITION NF105E08IR1F1067 Irradiated Medicago truncatula cDNA clone  
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 VERSION B0157500.1 GI:20294559  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.  
 1 (bases 1 to 466)  
 REFERENCE Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula irradiated library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA

